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IFNRELKI 394	PLVDKWNVERLTGLSDEGR	HANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRK 	SFQERATFI SFQERATFI	IPDDYFVVLVGDMITEBALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTA :	PNLQVTHSMPPOKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVR RPEVDELFNSLEGWARDNILVHLKSVENSWQPQDYLPDPTSDAFEDQV	NSMVLDNLK : : SPLVFDKLK	DB 2; Length 385; -105; 36; Indels 31; Ga	9.2) - cc 4 #text_c 4 #text_c 92 92 92 454797 454797 454797	tryptophan synthas restriction modifi restriction modifi restriction modifi hypothetical prote cyclin E - Caenorh hypothetical prote hypothetical prote tryptophan synthas HsdMl protein - My acetyltransferase hypothetical prote probable polyketid hypothetical prote ankyrin-like prote mitotic spindle as hypothetical prote mitotic spindle as hypothetical prote
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R;Chen, B.
submitted
                                 acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precus N;Alternate names: stearcyl-acyl carrier protein desaturase C:Species: Glycine max (soybean) C:Date: 14-May-1999 #sequence_revision 14-May-1999 #text_chec:Accession: T07806
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Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991
A:Title: Stearoyl-acyl-carrier-protein desaturase
A:Reference number: A39170; MUID:91172837; PMID:20
A:Accession: A39170
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A; Residues: 1-396 < SHA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A:Molecule type: mRNA
A:Residues: 1-396 <KNU>
A:Cross-references: EMBL:X56508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor N;Alternate names: stearoyl-[acyl-carrier-protein] desaturase C;Species: Ricinus communis (castor bean) C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 #text_change C;Accession: S16463; A39170
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C;Accession: S16463; A39170
R;Knutzon, D.S.; Scherer, D.E.; Schreckengost,
Plant Physiol. 96, 344-345, 1991
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Pred. No. 3.1e-101;
""ematches 52;
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F;36-399/Product: acyl-[acyl-carrier-protein] desaturase #status
                                                                                                                                                                                                                                                                                                                                                   acyl-[acyl-carrier-protein] desaturase (EC 1.14.19. N;Alternate names: Stearcyl-(acyl-carrier-protein] C;Species: Spinacia oleracea (spinach) C;Date: 31-Dec-1992 #sequence_revision 31-Dec-1992 C;Accession: S22480; S18183
                                                                                                                                                                                                                                    A; Residues:
                                                                                                                                                                                                                                                 A; Molecule type: mRNA
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A;Title: Nucleotide sequence of a CDNA clone encoding a A;Reference number: S22480; MUID:92329733; PMID:1627785
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C:Superfamily: acyl-[acyl-carrier-protein] desaturase
C:Keywords: chloroplast; oxidoreductase
F:1-29/Domain: transit peptide (chloroplast) #status |
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A;Accession: T07806
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-411 <CHE>
A;Cross references: EMBL:L34346; NID:g508602; PIDN:AAA92462.1; PID:g508603
C:Genetics:
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MALNLNDVSTPFQCRR--LPSFSPRQTPSRR--SPKFFMASTLSSSSPKEAESLKKPFSP
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C;Superfamily: acyl-[acyl-carrier-protein] desaturase
C;Keywords: chloroplast; oxidoreductase
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Proc. Natl. Acad. Sci. U.S.A. 88, 2510-2514, 1991
A;Title: Stearoyl-acyl-carrier-protein desaturase from higher
A;Reference number: A39170; MUID:91172837; PMID:2006187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acyl-{acyl-carrier-protein} desaturase (EC 1.14.19.2)
C;Species: Cucumis sativus (cucumber)
C;Date: 24-Jan-1992 #sequence_revision 24-Jan-1992 #te
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                                                                                                                                                                                                                                                                      VELRERAKELPDEYEVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTPWAIWTRAWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MALKLNFQCKKNHPAAFAKSPLPVTR-----VSSPRVFMASTVNSNSMVLDNLKSP---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RKAQEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI
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     RKAQEYVCELGPKIRRVEEKVQGKEKKKKAEHP-VSFSWIFNRELKI
                                                                 KKITMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEG
                                                                                                                                      ISHANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMR
                                                                                                                                                                                                                 AEENRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATF
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                                           KKVSMPAHLMYDGRDDNLFHHFSAVAQRLGVYTAKDYADILEFLVGRWKVESLTGLSGEG
                                                                                                                                                                                               AEENRHGDLLNKYLYLSGRVDMRQVEKTIQYLIGSGMDPRTENNPYLGFIYTSFQERATF
                                                                                                                                                                                                                                                                                                                                                  PREVHLQVTHSMPPQKMEIFKSLEDWAEENLLVHLKPVERCWQPQDFLPDSAFEGFHEQV
                                                                                                                                                                                                                                                                                                                                                                                       ---PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQV 108
                                                                                                                                                                                                                                                                                                                                                                                                                               MALKF------HPLTSQSPKLPSFRMPQLASLRSPKFVMASTLRSTSREVETLKKPFMP
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                                                                                                                    ISHGNTARLAKEHGDIKLAQICGTITADEKRHETAYTKIVEKLFEIDPEGTVIAFEDMMR
                                                                                                                                                                                                                                                                                                            RELRERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWT 168
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271; Conserv
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66.6%;
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A;Status: preliminary
A:Status: preliminary; nucleic acid sequence not shown; translation not shown A:Molecule type: mRNA A:Residues: 1-398 
A:Residues: 1-398 
A:Cross-references: EMBL:X60978; NID:g17928; PIDN:CAA43294.1; PID:g17929
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1991
C:Superfamily: acyl-lacyl-carrier-protein] desaturase
C:Keywords: chloroplast; oxidoreductase
                                                                                                                                acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) pr C;Species: Brassica rapa (turnip) C;Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text C;Accession: S23351 F.Knutzon, D.S.; Thompson, G.A.; Radke, S.E.; Johnson, W. Proc. Natl. Acad. Sci. U.S.A. 89, 2624-2628, 1992 A;Title: Modification of Brassica seed oil by antisense A;Reference number: S23351 MUID:92212881; PMID:1557366 A;Accession: S23351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:M61109; NID:g167196; PIDN:AAA3 C;Superfamily: acyl-[acyl-carrier-protein] desaturase C;Keywords: chloroplast; oxidoreductase
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C;Species: Carthamus tinctorius (safflower);
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 03-Jun-2002
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A; Residues: 1-396 <THO>
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                                                                                                                                                                                                                                                                                                                                                                                                             GNTARHAKDHGDVKLAQICGTIASDEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKI
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Pred. No. 4.2e-95;
4; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIDN: AAA33021.1;
                                                                                                                                                                                                             Johnson, W.B.; Knauf, V.C.; Kridl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S.; Kenny, J.W.; Young, H.L.;
                                                                                                                                                                                                                                                   #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                        precursor -
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C;Superfamily: acyl-[acyl-carrier-protein] desaturase
C;Keywords: fatty acid biosynthesis; oxidoreductase
                                                                                                                                                                                                                                                                                                                 A; Experimental source: strain C; Function:
                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-396 <HON>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                                        R;Hongtrakul, V.; Slabaugh, M.B.; Knapp, S.J. submitted to the EMBL Data Library, February 1997 A;Description: Sunflower stearoyl-ACP desaturase. A;Reference number: 217946
                                                                                                                                                                                                                                                                                                                                                                               A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: T14264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C:Species: Helianthus annus (common sunflower)
C:Date: 20-Sep-1999 #sequence revision 20-Sep-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2)
N;Alternate names: stearyl-ACP desaturase
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LLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISHANTAK
                              EIPDEYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTPWAIWTRAWTAEENRHGD
                                                EIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEENRHGD
                                                                                    THSMPPOKLEIFKSLDDWARNNVLIHLKSVEKSWQPODYLPDPVSDGFEEQVRELRERAK 116
                                                                                                                                              ALRMSPVTLQREIYPSYTFHQSKNLRSPKFAMASTIGSSTPKVESTKKPFTPPREVHLQV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NTARQAKEHGDLKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVMAFADMMRKKIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENNPYLGFIYTSFQERATFISHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HVQVLHSMPPQKIEIFKSMEDWAEQNLLTQLKDVEKSWQPQDFLPDPASDGFEDQVRELR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MALKLNFQCKK--NHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269;
                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                    EMBL: U91339; NID: g2290399; PID: g2290400
                                                                                                                                                                                                                           67.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            67.7%;
                                                                                                                                                                                                                                                                                                                             Mammoth
                                                                                                                                                                          ----VSSPRVFMASTVNSNSMVLDNLKSP-----PNLQV 56
                                                                                                                                                                                                             52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55;
                                                                                                                                                                                                                         Score 1395;
Pred. No. 2
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                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                        .7e-94;
ies 56;
                                                                                                                                                                                                                                       DB 2;
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                                                         176
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   236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Genome: nuclear C;Superfamily: acyl-[acyl-carrier-protein] desaturase C;Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase F;1-30/Domain: transit peptide (chloroplast) #status predicted <
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;31-393/Product: acyl-[acyl-carrier-protein] desaturase #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted to the EMBL Data Library, A; Reference number: S44202
A; Accession.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      acyl-[acyl-carrier-protein] desaturase (EC 1.14.19 N;Alternate names: stearyl-ACP desaturase C;Species: Solanum commersonii (Commerson's wild pc C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 C;Accession: S44202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:X78935; NID:g474832; PIDN:CAA55535.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-393 <TRU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Accession: S44202
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                                                                                                                                                                                                                                                                                                                                                                                                1 MALKLN---FOCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLK---SPP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                         local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Match
                         QEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI 394
                                                                         TMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKA 351
                                                                                                                    GNTARHAKEHGDMKLAQVCGIIAADEKRHETAYTKIVEKLFEVDPDGTVLAVADMMRKKI
                                                                                                                                                                                                 NRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISH
                                                       SMPAHLMYDGRDDNLFEHFSTVAQRLGVYTAKDYADILEFLVGRWEIEKLTGLSGEGHKA
                                                                                                                                      ANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMYRKKI
                                                                                                                                                                                NRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENNPHLGFIYTSFQERATFISH
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 RDYVCGLAPRIRKLEERAQARAKQKA-
                                                                                                                                                                                                                                            RERCKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTPWAIWTRAWTAEE
                                                                                                                                                                                                                                                             RERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEE
                                                                                                                                                                                                                                                                                                                            -NLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVREL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                          267;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLYDKWNVERLTGLSDEGRKAQEYVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKITMPAH
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66.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.; Leone, A.
ry, April 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1386.5; DB 2;
Pred. No. 1.1e-93;
3; Mismatches 64;
-PVPFSWVFGKDIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (EC 1.14.19.2) precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 potato)
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393
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                                                                                                                                                                                                                                                                                                                                                                                                                                  19;
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g

RESULT 10 S24995 acyl-[acyl-carrier-protein]

desaturase

(EC

1.14.19.2) precursor -

rape

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C: Accession: T07653
C: Accession: T07653
R:Taylor, M.A.; Smith, S.B.; Davies, H.V.; Burch, L.R.
submitted to the EMBL Data Library, April 1992
A;Description: The primary structure of a cDNA clone o
A:Reference number: Z16073
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Mol. Biol. 20, 151-155, 1992
A;Title: Nucleotide sequence and temporal regulation of a A;Reference number: S24995; MUID:92385757; PMID:1515603
A;Accession: S24995
                             C; Function: A; Description: catalyzes the formation of double bonds at the delta(9) C; Superfamily: acyl-[acyl-carrier-protein] desaturase C; Keywords: chloroplast; fatty acid biosynthesis; oxidoreductase
                                                                                                                                                                                           A;Reference number: Z16073
A;Accession: T07653
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) precursor - N;Alternate names: stearoyl-acyl carrier protein desaturase C;Species: Solanum tuberosum (potato) C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 0:
                                                                                                                                                                                                                                                                                                                                                                                        RESULT
T07653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X63364; NID:g17869; PIDN:CAA44964.1; PID:g17870 C;Superfamily: acyl-[acyl-carrier-protein] desaturase C;Keywords: chloroplast; fatty acid biosynthesis; homodimer; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N:Alternate names: stearoyl-[acyl-carrier-protein] desaturase
C:Species: Brassica napus (rape)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 03-Jun-2002
C:Accession: S24995
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A; Residues: 1-399 <SLO>
                                                                                                                 A; Genome: nuclear
                                                                                                                                                 A;Cross-references:
                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-393 <TAY>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TMPAHLMYDGSDELLFKHETAVAQRVXVYSALDYCDILEFLYDKWNVERLTGLSDEGRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVREL 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEYLCGLTPRIRRLDERAQARAKKGP---KIPFSWIHDREVQL 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMPAHLMYDGRDDNLFDNESSVAQRLGVYTAKDYADILEFLAGRWRIESLTGLSGEGNKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENNPYLGFIYTSFQERATFVSH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MALKENPLVSQPYKLASSARP-PVSTFRSPKFLCLASSSSPALSSKEVESLKKPFTPPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    265;
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Similarity
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                                                                                                                                                 EMBL: M91238;
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67.2%;
64.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59; Mismatches
                                                                                                                                               NID:g169564; PIDN:AAA33839.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1386.5;
Pred. No. 1.1
Score
Pred.
No. 1.3e-
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DB 2;
-93;
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            Length 393;
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                                                                                                                                               PID:g169565
                                                                                                                                                                                                                                                                                                                  03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                    potato
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                                                                              position
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EENRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENNPYLGFIYTSFQERATFI EENRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFI

239

60 52

--PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVR 109

REVHVQVLHSMPPQKIEIFKSMENWAEENLLIHLKDVEKSWQPQDFLPDPASDGFEDQVR

119

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stearoyl-ACP desaturase [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: E84869
                                                                                                                                                    A;Gene: At2g43710
A;Map position: 2
C;Superfamily: acyl-[acyl-carrier-protein] desaturase
                                                                                                                                                                                                                                                                                                      A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: E84869 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                      R;Lin, X.; Kaul, S.; Rouns
M.; Koo, H.; Moffat, K.S.;
euss, D.; Nierman, W.C.; W
                                                                                                                                                                                                                         A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                   A; Residues: 1-401 <STO>
                                                                                                                                                                                                                                                                                                                                                                                          Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
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                                                                                                    Query Match
Best Local
                                                                                   Matches
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                                                                                                    Local Similarity
    _
                                         1 MALKLNFQCKKNHPAAFAKSPLPVT-RVSSPR-VFMAST---VNSNSMVLDNLKSP----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKAQEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GDLLNKYLYLSGRVDMKQIEKTIQYLIGSGMDPRTENNPYLGFVYTSLRKGVTFVSHGNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEENRH 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELRER 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MALKLNFQCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLK---SPP---NL 54
MALKEN-PLVASQPYKEPSSTRPPTPSFRSPKFLCLASSSPALSSGPKEVESLKKPETPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISHANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QVTHSMPPEKIEVFDSLRDWAAQNLLVHLKPVEKCWQPTDFLPDPASEGFDEQVKELRER 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MALNINGVSLKSHKML----PFPCSSARSERVFMASTIHRPSVEVGSVKKAFTPPREVHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VCGLAPRIRKLEERAQARAKHAKS---VPFSWIFGKEIKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AHLMYDGRDDNLFEHFSAVAQRLGVYTAKDYADILEFHVGRWEVEKLTGLSSEGRRAQDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258;
                                                                                   266;
                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii,
                                                                                                                                                                                                                                              GB:AE002093; NID:g2281099; PIDN:AAB64035.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                         .S.; Cronin, L.A.; Shen, M.; VanAken ; White, O.; Eisen, J.A.; Salzberg,
                                                                                                    67:0%; Score 1381.5; 65.7%; Pred. No. 2.66
                                                                               61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62;
                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                 .5; DB 2;
2.6e-93;
nes 63;
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                                                                                   Indels
                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                           S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                             S.E.;
                                                                                 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                Umayam,
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    59
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C.Y

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RESULT
acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2)
N;Alternate names: delta 9 stearoyl-[acyl-carrier prot
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                                                                                                                                   Qy
                                                                                                                                                                      Вb
                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                     DЪ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Description: introduces a double bond at the delta(9)
A;Pathway: fatty acid biosynthesis
C;Superfamily: acyl-[acyl-carrier-protein] desaturase
C;Keywords: fatty acid biosynthesis; oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Hongtrakul, V.; Slabaugh, M.B.; Knapp, S.J. submitted to the EMBL Data Library, February 1997 A;Description: Sunflower stearoyl-ACP desaturase. A;Reference number: Z17946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acyl-[acyl-carrier-protein] desaturase (EC 1.14.19
N;Alternate names: stearoyl-ACP desaturase
C:Species: Helianthus annuus (common sunflower)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
T14268
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A;Experimental source: strain Mammoth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 C:Accession: T14268
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Best Local
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                                                                                                                                                                                       TMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKA
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                                                                                                                                      QEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI 394
                                                                                                                                                                     {\tt GNTARHAKEHGDVKLAQMCGIIAADEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKII}
                                                                                                                                                                                                                                                        ANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKI
                                                                                                                                                                                                                                                                                                                     NRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NRHGDLLHQYLYLSGRVDMRQIQKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFISH
                                                                                                                                                                                                                                                                                                                                                                                                  RERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MALKLN----FQCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KAQDYLCGLAPRIKRLDERAQARAKKGP---KIPFSWIHDREVQL 401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAIRINTATEQSDLYRSFAFPQ-PKP---LRSPKFAMASTIGSATTKVESTKKPFTPPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KAQEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SHANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SHGNTARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVMAFADMMRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                67.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Score 1381; DB 2;
; Pred. No. 2.8e-93;
54; Mismatches 65
     9.2) precursor protein] desa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65;
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acyl-[acyl-carrier-protein] desaturase (EC 1.14.19.2) - common sunflower N;Alternate names: Stearcyl-ACP desaturase C:Species: Helianthus annuus (common sunflower) C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 03-Jun-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Gossyplum nirsucum
C;Jate: 16-Jul-1999 #sequence
C;Accession: T10793
R;Liu, Q.; Singh, S.; Sharp,
Plant Physiol. 110, 1436, 199
Plant Physiol. 110, 1436, 199
C; Function:
A; Description:
                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, Se
A;Description: Sunflower stearoyl-ACP
A;Reference number: Z17901
                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-396 <COU>
                                                                                                                                                                                                                           A; Reference number: A; Accession: T14172
                                                                                                                                                                                                                                                                                                                                                   C; Accession: T1417
R; Coughlan, S.J.;
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                                                                  A; Experimental
                                                                                             A;Cross-references: EMBL:U70374; NID:g1575696; PID:g1575697
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A; Residues: 1-397 <LIU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references:
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Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
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      introduces
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7.1e-93;
hes 76;
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C; Superfamily: acyl-[acyl-carrier-protein] desaturase
C; Keywords: fatty acid biosynthesis; oxidoreductase
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Search completed: December Job time : 23 secs

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Maximum Match 100%
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Sequence:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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6: /cgn2_6/ptodata/1
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Match
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/cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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US-08-474-587-6
US-08-471-91-13
US-08-926-522-2
PCT-US91-01746-13
US-08-926-522-6
US-08-926-522-6
PCT-US91-01746-20
                   US-08-869-137-2

US-08-39-798-2

US-08-329-560-2

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US-09-422-662-19

US-08-917-299-34

US-09-422-662-34

US-08-917-299-3

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                             Sequence 16, Appli
Sequence 1, Appli
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Sequence 13, Appli
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	Sequence 7, Appli	Sequence 7, Appli	Sequence 14, Appl	Sequence 14, Appl	`	Sequence 17, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 18, Appl	`	`	`	`	`	•	Sequence 12, Appl	`

ALIGNMENTS

RESULT 1 US-08-539-798-4

Sequence 4, Application US/08539798 Patent No. 5614400

GENERAL INFORMATION:

NUMBER OF SEQUENCES:

APPLICANT: CAHOON, Edgar B.
APPLICANT: OHLROGEE, John B.
TITLE OF INVENTION: Methods and Compositions Relating to
TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase

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                                                   Matches
                                                                 Query Match
Best Local
                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/539,798
                                                                                                                                                                                                                                    REGISTRATION NUMBER: 36,063
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4844
                                                                                                                                                                                                                                                                                                                     FILING DATE: 26-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Yates, Michael E.
                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/329,560
FILING DATE: 26-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Pioneer Hi-Bred International, Inc
STREET: 700 Capital Square, 400 Locust Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 700 Capita
CITY: Des Moines
STATE: Iowa
COUNTRY: US
ZIP: 50309
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: CLASSIFICATION:
                                                 Local Similarity
les 296; Conserv
                                                                                                                              STRANDEDNESS:
TOPOLOGY: linear
                                                                                                                                                                     TYPE:
                                                                                                                                                                                   LENGTH:
                 1 MALKLN----FQCKKNHPAAFAKSPLPVTRVSSP-----RVFMASTVNSNSMVLDNLK 49
                                                                                                                                                                   amino acid
                                                                                                                                                                                     385 amino acids
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                               800
                                                                 74.9%;
                                                 42;
                                               Score 1544.5;
Pred. No. 2.2e-
42; Mismatches
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Matches 296;
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: CAHOON, Edgar B.
APPLICANT: OHLEGGEE, John E
                                                                                                                                                              TELEFAX: (515) 248-4844 INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIDIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: OHLROGEE, John B.
TITLE OF INVENTION: Methods and Compositions Relating to
TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier
                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Yates, Michael E.
REGISTRATION NUMBER: 36,063
REFERENCE/DOCKET NUMBER: 021
                                                                                                                                                                                                                                                                                                            SOFTWARE: Patentin Relaction DATA:
                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 385 amino acids
                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (515) 248-4800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/329,560 FILING DATE: 26-OCT-1994 CLASSIFICATION: 435
                                                                                                          STRANDEDNESS:
                                                                                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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  1 MALKLN--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAQEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ELRERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPPNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVR 109
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                                          Similarity
                                                                                                                       amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                              3: Pioneer Hi-Bred International, Inc
700 Capital Square, 400 Locust Street
                              Conservative
                                                                                             linear
  -FQCKKNHPAAFAKSPLPVTRVSSP---
                                          74.9%;
73.1%;
                             42;
                            Score 1544.5;
Pred. No. 2.2e
l2; Mismatches
                                                                                                                                                                                                                   0284US
                                                                                                                                                                                                                                                                                                                            Version
                                           2.2e-148;
    ---RVFMASTVNSNSMVLDNLK 49
                                                        DB 1;
                              36;
                              Indels
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                              31;
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US-08-539-798-3
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; Patent No. 5614400
; GENERAL INFORMATION:
TOPOLOGY: US-08-539-798-3
                                                                                                                                               FILING DATE: 26-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Yates, Michael E.
REGISTRATION NUMBER: 36,063
REFERENCE/DOCKET NUMBER: 0.84
TELECOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPHONE: (515) 248-4844
                                                                                                                               TELEFAX: (515) 248-4844
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 800
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
COFFMANDE: Datasett Belleri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: CAHOON, Edgar B.
APPLICANT: OHLROGEE, John B.
TITLE OF INVENTION: Methods and Compositions Relating to
TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                       SEQUENCE CHARACTERISTICS:
                                                             LENGTH:
TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Des Moines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Pioneer Hi-Bred International, Inc
STREET: 700 Capital Square, 400 Locust Street
                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KAQEYVCSLAAKIRRVEEKVQGKE--KKAVLPVAFSWIFNRQIII 385
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EENRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFI 229
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                                                               amino acid
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                                                                                  396 amino acids
                     linear
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                                                                                                                                                                                                                                                                                                                                    us 08/329,560
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Score 1490;

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Length

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US-08-329-560-3
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TOPOLOGY: US-08-329-560-3
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Patent No. 5654402
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: CAHOON, Edgar B.
APPLICANT: OHLROGEE, John B.
TITLE OF INVENTION: Methods and Compositions Relating to
TITLE OF INVENTION: Plant 6-Delta Palmitoyl-Acyl Carrier Protein Desaturase
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                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Yates, Michael E.
REGISTRATION UNMBER: 36,063
REFERENCE/DOCKET NUMBER: 0284
TELEOMMUNICATION INFORMATION:
TELEPHONE: (515) 248-4800
TELEPAX: (515) 248-4844
                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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ADDRESSEE: Pioneer H
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CITY: [
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                                   STRANDEDNESS
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                                                                   LENGTH:
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YVCRLPPRIRRLEERAQGRAK----EAPTMPFSWIFDRQVKL 396
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                                               : 396 amino acids amino acid
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                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                linear
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                                                                                                                                                                                                                                                                                                                                                                           Floppy disk
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Best Local Similarity 71.1
Matches . 286; Conservative
                                                                                                                                                                                          COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: MicrosoftWord 5.1 (a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,791
FILING DATE: 6-JUNE-95
CLASSIFICATION 135
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/762,762
FILING DATE: 16-SEPT-1991
CLASSIFICATION. 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
COMPUTER: Apple Macinto
                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                  PRIOR APPLICATION DATA:
                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Plant Desaturases-Compositions TITLE OF INVENTION: and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thompson, GreatPLICANT: Knauf, Vic C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        239
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                                                                                                      APPLICATION NUMBER: FILING DATE: 14-MA CLASSIFICATION: 43
                                                   APPLICATION NUMBER: 07/615,784 FILING DATE: 14-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Davis
STATE: Cali
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               APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           59 VQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKCWQPQDFLPDPASDGFDEQVRELRE 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        E: Calgene, Inc.
1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thompson, Gregory A
                                                                                                                       14-MAR-1991
13-AUG-1990
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71.1%; Pred. No. 8e-143;
                                                                                                                                            PCT/US91/01746
                 07/567,373
                                                                                                                                                                                                                                                                                         US/08/471,791
                                                                                                                                                                                                                                                                                                                                                                                  3.50 inch,
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Sequence 4, Application US/08926522
Patent No. 64.25447
GENERAL INFORMATION:
APPLICANT: Vic C. Knauf
APPLICANT: Gregory A. Thompson
TITLE OF INVENTION: PLANT SEED OF
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                       US-08-926-522-4
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COMPUTER READABLE FORM:
                                                                                                  CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acid
             COUNTRY: US
                                                                                                                                                                                                                                                                                                354 YVCELGPKIRRVEEKVQGKEKKKAEHP-VSFSWIFNRELKI 394
                                                                                                                                                                                                                                                                                                                                             299
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NAME: Lassen, Elizabeth
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                                              STATE:
                                                             CITY:
                                                                        STREET:
                                                                      ADDRESSEE: Calgene, Inc. STREET: 1920 Fifth Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Donna E. Scherer REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                      PAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKAQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQDQDYLPDPVSDGFEEQVRELRE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MALKLNPFLSQTQKLPSFALPPMASTR--SPKFYMASTLKSGSKEVENLKKPFMPPREVH
                                                                                                                                                                                                                                                                              PAHLMYDGRDDNLFDHFSAVAQRLGVYTAKDYADILEFLVGRWKVDKLTGLSAEGQKAQD
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N FOR SEQ ID NO: 16:
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RESULT 7
PCT-US91-01746-16
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                                                                                               Sequence 16, Application PC/TUS9101746 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
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INFORMATION FOR SEQ ID NO:
             TITLE OF INVENTION: Plant Desaturases-Compositions NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
                                                        APPLICANT: Thompson, Gregory A APPLICANT: Knauf, Vic C
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ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Carl J. Schwedler REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 3 NAME: Donna E. Scherer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 08/4 FILING DATE: 2-June-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MALKLN-FQCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----PN 53
                                                                                                                                                                                                                                                                                                                                           TAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKITM
                                                                                                                                                                                             YVCRLPPRIRRLEERAQGRAK----EAPTMPFSWIFDRQVKL
                                                                                                                                                                                                                                                          VQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKCWQPQDFLPDPASDGFDEQVRELRE 118
                                                                                                                                                                                                                            YVCELGPKIRRVEEKVQGKEKKKKAEHP-VSFSWIFNRELKI 394
                                                                                                                                                                                                                                                                                         PAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKAQE 353
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                                                                                                                                                                                                                                                                                                                                                                                           HGDLLNKYLYLSGRVDMRQTEKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFISHGN 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            286;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        72.3%; Score 1490; DB 4; Length 396; 71.1%; Pred. No. 8e-143;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 16:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/017
FILING DATE: 19910314
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: 07/615,784
FILING DATE: 14 NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CG:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintos
SOFTWARE: MicrosoftWord 4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 07/567;373
FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein
                                                                                                                                                                      239
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    359
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                                                                                                     PAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKAQE 353
                                                                                                                                                                                        TAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKITM
                                                                                                                                                                                                                                                                                                                                                                                                                                             LQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELRE 113
VVCRLPPRIRRLEERAQGRAK----EAPTMPFSWIFDRQVKL
                                         YVCELGPKIRRVEEKVQGKEKKKKAEHP-VSFSWIFNRELKI 394
                                                                                                                                                                  TARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKISM
                                                                                                                                                                                                                                                                          HGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISHAN 233
                                                                                                                                                                                                                                                                                                                                     RAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAEENR 178
                                                                                                                                                                                                                                                                                                                                                                                                                     VQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKCWQPQDFLPDPASDGFDEQVRELRE 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MALKLNPFLSQTQKLPSFALPPMASTR--SPKFYMASTLKSGSKEVENLKKPFMPPREVH 58
                                                                                    PAHLMYDGRDDNLFDHFSAVAQRLGVYTAKDYADILEFLVGRWKVDKLTGLSAEGQKAQD
                                                                                                                                                                                                                                                    HGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFISHGN
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                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 69.7%; Score 1436.5; DB 1; Best Local Similarity 68.5%; Pred. No. 2.1e-137; Matches 278; Conservative 44; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 6, Application US/07995657 Patent No. 5443974
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: GEIGER, KATHLEEN W.
REGISTRATION NUMBER: 35,8
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 19921211
FILING DATE: 0921211
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
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LENGTH: 391 amino acid
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ADDRESSEE: E. I. du
ADDRESSEE: and Compa
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TITLE OF INVENTION:
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OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft
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                                                                                                                                                                                                  QVRELRERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRA 166
                                                                                                                                                                                                                                                                            -----PNLQYTHSMPPQKLEIFKSLDDWARNNYLIHLKSVEKSWQPQDYLPDPVSDGFEE 106
                                                                                                           MALRLN------PIPTQTFSLPQMPSLRSPRFRMASTLRSGSKEVENIKKPF 46
MRKKITMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSD
                                     TFISHGNTARLAKEHGDIKLAQICGMIASDEKRHETAYTKIVEKLFEVDPDGTVMAFADM
                                                                       TFISHANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADM 286
                                                                                                                                               WTAEENRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERA 226
                                                                                                                                                                                   QVKELRERAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTSWAIWTRA 166
                                                                                                                                                                                                                                                           TPPREVHVQVTHSMPPQKIEIFKSLEDWADQNILTHLKPVEKCWQPQDFLPDPSSDGFEE
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US-08-474-587-6
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TELEX: 835420
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: SIEGELL, BARBARA C.
REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB_1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
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APPLICANT: Hitz, William D
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CURRENT APPLICATION DATA:
APPLICATION MINISTER STATEMENT APPLIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 391 amino acids
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CLASSIFICATION: 435
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                           QVRELRERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRA 166
                                                                                                                                                                                                                                                               MALKLNFQCKKNHPAAFAKSPLPYTRVS------SPRVFMASTVNSNSNV/LDNLKSP- 51
QVKELRERAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTSWAIWTRA
                                                                                                                                                 -----PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEE 106
                                                                                                                                                                                                                                   MALRIN------PIPTQTFSLPQMPSLRSPRFRMASTLRSGSKEVENIKKPF 46
                                                                                                                TPPREVHVQVTHSMPPQKIEIFKSLEDWADQNILTHLKPVEKCWQPQDFLPDPSSDGFEE 106
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278; Conserv
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Perez_Grau, Luis
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68.5%;
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Pred. No. 2.1e
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RESULT 10
US-08-471-791-13
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                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: PCT/US91/vi
FILING DATE: 14-MAR-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Plant Description of INVENTION: and Uses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                      PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Thompson, Gregory A APPLICANT: Knauf, Vic C
                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (916) 753-6313
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: MicrosoftWord 5.1 (a)
                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/50 FILING DATE: 13-AUG-1990
                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 14-NOV
                                                                  REFERENCE/DOCKET NUMBER:
                                                                                     NAME: Carl J. SchwereGISTRATION NUMBER:
                                                                                                                   NAME: Donna E. Scherer REGISTRATION NUMBER: 3
                                                                                                                                                    NAME: Lassen, Elizabeth REGISTRATION NUMBER: 31
                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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NE: (916) 753-6313
: (916) 753-1510
350370 CGNE
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RESULT 11
US-08-926-522-2
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Patent No. 6426447
GENERAL INFORMATION:
APPLICANT: Vic C. Knauf
APPLICANT: Gregory A. Thompson
TITLE OF INVENTION: PLANT SEED OILS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 68.2%;
Best Local Similarity 67.1%;
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                                                                                                                                           OPERATING SYSTEM: Macintosh 7.1 SOFTWARE: Microsoft Word 5.1(a) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS: ADDRESSEE: Calgene,
                         FILING DATE: 2-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    297
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                               COMPUTER: Apple Macintosh OPERATING SYSTEM: Macinto:
                                                                                                                                                                                                                                             ZIP:
REGISTRATION NUMBER: 3 NAME: Donna E. Scherer
                                                                        APPLICATION NUMBER:
                                                                                                                      FILING DATE:
                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                     CITY: Davis
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                                                                                                                                                                                                                                          95616
                                                                                                                                                                                                                                                                          CA
                                                                                                                                                                                                                                                                                                        1920 Fifth Street
                                                                                                                                                                                                                                                                                                                      Inc
                                                                                                                                   US/08/926,522
                                                                          08/458,173
              31,845
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                                                                                                                                                                                                              3.50 inch,
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                                                                                                                                                                                                                                                                                                                                                    Sequence 13, Application PC/TUS9101746 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
              SOFTWARE: MicrosoftWord 4.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US91 FILING DATE: 19910314
                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                                                                                           APPLICANT: Thompson, Gregory A
APPLICANT: Knauf, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                          STREET: 1920
CITY: Davis
STATE: Calif
                                                                                                                                                                                                                                                                                                                                                                                                                                                            357
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                                                                 COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintos SOFTWARE: MicrosoftWord 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE:
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FILING DATE: 19
CLASSIFICATION:
                                                                                                                                                         COUNTRY: USA
ZIP: 95616
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                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MALKL---NFQCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          QDYVCGLPPRIRRLEERAQGRAK----EGPVVPFSWIFDRQVKL
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1920 Fifth Street
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                                                                                      Macintosh 6.0.7
                                    PCT/US91/01746
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                                                                                                                      3.50 inch,
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Pred. No. 2.7e-134;
                                                                                                                        1.0
                                                                                                                        MB storage
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RESULT 13
US-08-471-791-20
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                                                                                                                                                                               Sequence 20, Application US/0847179: Patent No. 5723595
                                                                                                                                                                             Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                GENERAL INFORMATION:
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TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 396 amino acids
                                                                    TITLE OF INVENTION: Plant De:
TITLE OF INVENTION: and Uses
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
                                                                                                                              APPLICANT: Thompson, Gregory A APPLICANT: Knauf, Vic C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: protein
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REFERENCE/DOCKET NUMBER: CGNE
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 07/A9
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
              ADD.
STREET:
Davis
Cali
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Lassen, Elizabeth REGISTRATION NUMBER: 31
COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                    QEYVCELGPKIRRVEEKVQGKEKKKKAEHP-VSFSWIFNRELKI 394
                                                                                                                                                                                                                                                                                                                                                                                                         ANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKI 291
                                                                                                                                                                                                                                                                                                                                                                                        GNTARHAKDHGDVKLAQICGTIASDEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                RERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEE 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVREL 111
                                                                                                                                                                                                                                                                      QDYVCGLPPRIRRLEERAQGRAK----EGPVVPFSWIFDRQVKL 396
                                                                                                                                                                                                                                                                                                                              SMPAHLMYDGRDDNLFEHFSAVAQRLGVYTAKDYADILEFLVGRWKVADLTGLSGEGRKA
                                                                                                                                                                                                                                                                                                                                                TMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKA 351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               {\tt RARAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTPWAVWTRAWTAEE}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VHVQVTHSMPPQKIEIFKSIEGWAEQNILVHLKPVEKCWQAQDFLPDPASEGFDEQVKEL 116
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            California
                                        E: Calgene, Inc.
1920 Fifth Street
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67.1%;
                                                                                                                Plant Desaturases-Compositions
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Pred. No. 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (916) 753-151
TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 16-MAR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/762,762
FILING DATE: 16-SEPT-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
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                   293
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Lassen, Elizabeth REGISTRATION NUMBER: 31
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FILING DATE: 16-MAR-1990
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FILING DATE: 13-AUG-1990
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MPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKAQ
                                                                                                                                                                                           ERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGABPSAWAMWTRAWTAEEN 172
                                                NTARQAKEHGDLKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVMAFADMMRKKIS
                                                                                                             RHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISHA
                                                                                                                                                                                                                                       {\tt HVQVLHSMPPQKIEIFKSMEDWAEQNLLTQLKDVEKSWQPQDFLPDPASDGFEDQVRELR}
                                                                                                                                                                                                                                                                                                     MALKLNPLASQPYNFPSS-ARPPISTFRSPKFLCLASSSPALSSKEVESLKKPFTPPKEV
                                                                              NTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKIT
                                                                                                                                                                           ERARELPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAEEN
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69; Conservative
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(916) 753-1510
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66.9%;
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Pred. No. 2.8e-133;
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Patent No. 6426447
GENERAL INFORMATION:
APPLICANT: Vic C. Knauf
APPLICANT: Gregory A. Thompson
TITLE OF INVENTION: PLANT SEED OILS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (916) 753-1510 INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,17
FILING DATE: 2-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: CG
                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 353 EYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI 394
     180
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OPERATING SYSTEM: Macinto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/926,522 FILING DATE:
                                                                                                                                                                    53 NLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELR 112
                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 1920
CITY: Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                     1 MALKLNFQCKK--NHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----P 52
                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH:
ERAKEIPDDYEVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEEN 172
                                                                ERARELPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAEEN
                                                                                                                                     HVQVLHSMPPQKIEIFKSMEDWAEQNLLTQLKDVEKSWQPQDFLPDPASDGFEDQVRELR 119
                                                                                                                                                                                                      MALKLNPLASQPYNFPSS-ARPPISTFRSPKFLCLASSSPALSSKEVESLKKPFTPPKEV 59
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CLASSIFICATION: 435
PRIOR APPLICATION DATA: 07/615,784
APPLICATION NUMBER: 07/615,784
FILING DATE: 14 NOV-1990
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 07/494,106
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: LASSEN, Elizabeth
                                                                                                                                                                                                                                                                                                                            TELEX: 350370 CGNE INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CC TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Thomps APPLICANT: Knauf,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Plant Desaturases-Compositions and Uses NUMBER OF SEQUENCES: 43
                                                                                                                                                                                                                                 MOLECULE TYPE:
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OPERATING SYSTEM: Macintosh
SOFTWARE: MicrosoftWord 4.0
                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
NAME: Donna E. Scher
REGISTRATION NUMBER:
                   53 NLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELR 112
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                                                     MALKLNPLASOPYNFPSS-ARPPISTFRSPKFLCLASSSPALSSKEVESLKKPFTPPKEV 59
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1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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(916) 753-1510
                                                                                                                                 Conservative
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Knauf, Vic C
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360 EYLCGLTPRIRRLDERAQARAKKGP---KVPFSWIHDREVQL 398
                           60 HVQVLHSMPPQKIEIFKSMEDWAEQNLLTQLKDVEKSWQPQDFLPDPASDGFEDQVRELR 119
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Search completed: December 1, 2002, 21:22:08 Job time : 20 secs

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Minimum
Maximum
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Perfect score:
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is derived by analysis of the total score distribution.
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ALIGNMENTS

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JOURNAL REFERENCE AUTHORS TITLE DEFINITION ACCESSION VERSION KEYWORDS REFERENCE AUTHORS SOURCE ORGANISM RESULT 1 AY104235 LOCUS FEATURES TITLE JOURNAL source Coe,E.C.
Direct Submission
Submitted (25-APR-2002) Maize Mapping Project,
Submitted (25-APR-2002) Maize Mapping Project,
Missouri, Columbia, MO 65211, USA
Location/Qualifiers Zea mays PC AY104235 AY104235.1 Zea mays Zea mays l (bases 1 to 1780)
Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S., Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
Maize Mapping Project/DuPont Consensus Sequences for Design of Overgo Probes Unpublished (2002) 2 (bases 1 to 1780) Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea. AY104235 PCO105183 mRNA sequence. /organism="Zea mays"
/db_xref="MaizeDB:636088"
/db_xref="taxon:4577"
/clone="PCO105183" 1780 bp mRNA University HTC 25-MAY-2002 of

Result No.

Score

Query Match

Length DB

IJ

Description

513 491.2 424.4 382.6 372.2 368.8

38.2 36.5 31.6 28.5 27.7 27.4

1780 1623 702 708 712 699

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AY104235 AY104301 BM436665 BI271942 BG269539 BU027980

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                                                                                                                                                                                                                             AAAGCTCGCTGAGATCGACCCCGACACACAGTAATTGCTTTTGCAGATATGATGCGCAA
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494 g 412 t
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Pred. No. 2.4e-97;
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                  AGAAGAAGCACTTCCAACATATATGTCTATGCTCAATAGGTGTGATGGTATTAAGGATGA
                                                 GGAGCGGGCAAATGAAATACCTGATGAATACTTTGTTTGCTTAGTTGGTGATATGGTTAC
                                                                GGAAAGGGCCAAGGAGATTCCCGACGACTATTTTGTGGTGTTTAGTTGGAGATÄÄGÄTCAC
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Zea mays PC
AY104301
AY104301.1
HTC.
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Spermatophyta; Magnoliophyta; Liliopsida;
clade; Panicoideae; Andropogoneae; Zea.
1 (bases 1 to 1623)
1 (bases 1 to 1623)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitsitt,M.S.,
Arthur,L.W., Hanafey,M., Morgante,M. and Tingey,S.V.
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 /note="this sequence is part of a project of EST assemblies resulting from the application of public contigs to seed DuPont contigs; this resource was assembled by DuPont as part of a collaboration for the overgo addressing of BACs in conjunction with the Maize Mapping Project" 376 c 445 g 361 t
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/db_xref="MaizeDB:633889"
/db_xref="taxon:4577"
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                                                                                                                                                                                                                                                                                                                                                             GAAGATATGAACAGGAAGGGAAGGGAATGGAGG
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                                                                                            Vitis vinifera
Eukaryota; Viridiplantae;
                                                                                                                                                                                                 PM436665 702 bp mRNA linear EST 31-JAN-2002 VVA008A04_52913 An expressed sequence tag database for abiotic stressed leaves of Vitis vinifera var. Chardonnay Vitis vinifera CDNA clone VVA008A04 5, mRNA sequence.
An expressed sequence tag data Vitis vinifera var. Chardonnay
                                 Cramer, G.R. and Cushman, J.C
                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e
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Tel: 775-784-1918
Fax: 775-784-1650
Email: jcushman@unr.edu
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Contact: Cushman
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TCTATGCTCAATAGGTGTGATGGTATTAAGGATGAGACTGGGGCTGAGCCCAGTGCTTGG
                                         GATTACTTTGTTGTTCTGGTTGGAGATATGGTCACAGAAGAAGCTCTTCCTACTTACCAA 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Torres-Jerez,I., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C., Flores,H.R., Inman,J.T., Weller,J.W. and May,G.D. Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula flower library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BI271942 708 bp NF016709F1F1078 Developing flower NF016F09FL 5', mRNA sequence. BI271942
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: gdmay@noble.org
Insert Length: 708 Std Error: 0.00
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                                                                                                                                                                                                                                                                                                                                                        /note="Vector: Lambda Zap; cDNA was prepared from polyAtenriched, pooled samples of equivalent amounts of total RNA from very young, developing, fully-pened flowers are flowers transitioning into pods. The cDNA was directionally ligated into the Uni-Zap XR vector (Strategene) and packaged using the Gigapack III Gold
                                                                                                                                                                                                                                                            packaging extracts. Phagemids containing cDNA inserts were in vivo excised from the recombinant Uni-ZAP XR vector using ExAssist helper phage and the E. coli strain XLI-Blue MRF' (Stratagene). Excised plasmids were plated using SOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Developmentally pooled. Contains a mixture of very young, developing, fully-opened flowers and flowers in early transition into pods."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Medicago truncatula"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Developing flowers"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Developing flower"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="NF016F09FL"
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                                                                                                                                                 28.5%;
71.0%;
                                                                                                                                                                                                                                                        SOLR cells
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                                                                                                                                              Score 382.6; DB 1
Pred. No. 5.1e-70;
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BG269539
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              PCR PRimers
FORWARD: T7
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BG269539.1
EST.
                                                                 MS200, Reno, NV 89557-0014, Tel: 775-784-1918
Fax: 775-784-1650
                                                                                  University of Nevada MS200, Reno, NV 8955 Tel: 775-784-1918
                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Aizoaceae; Mesembryanthemum.
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LO-3624T3 Ice plant Lambda Uni-Zap XR expression library, 0 hou
NaCl treatment Mesembryanthemum crystallinum cDNA clone LO-3624
                                                                                                                                                       Unpublished (1997)
Contact: Cushman J
                                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
BACKWARD:
                                                 Email: jcushman@unr.edu
                                                                                                                                        Department of Biochemistry
                                                                                                                                                                                                                              Cushman,
                                                                                                                                                                                                                                                                                                                  Mesembryanthemum crystallinum
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           AGATCGACCCCGA 875
                                                            TCGCCTCCGACGAGAAGCGCCACAGCCTACACCAAGATCGTGGAAAAGCTCGCTG
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                                                                                                                                                        CTTATCTTGGCTTCATATACACATCATTTCAAGAGAGAGCCACCTTTGTTTCCCATGGCA
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                                                                                                    ACACTGCAAGACATGCTAAGGAGCACGGGGATCTCAAGCTAGCACAGATGTGCGGTATAA
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Seq primer: T3
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ECORI; Site_2: XhoI"
147 c 172 g 181 t
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/tissue_type="Leaf"
/dev_stage="Six week old"
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/clone="L0-3624"
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72.18;
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 Mismatches

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RESULT 6 BU027980

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186
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                     TCCAACATATATGTCTATGCTCAATAGGTGTGATGGTATTAAGGATGAGACTGGGGCTGA
                                                                                                                                                                                                GCCGGATCCGGTGTCAGACGGATTCGAGGAGCAAGTGCGGGAGTTGAGGGAAAGGGCCAA 392
GCCTACTTACCAAACAATGCTTAATACTCTTGATGGTGTGCGTGATGAGACCGGGGCTAG
                                                                                                                                                          ACCAGATCCCGCATCTGACGGATTTATGGAACAAGTGGAGGAACTACGAGCTCGGGCTAA 125
                                                                                                                                                                                                                                           GAAGATACTATTGGTTCACCTAAAGCCCGTCGAAAAATGCTGGCAAGCACAGGATTTCCT
                                                                                                                                                                                                                                                                                                                         490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Department of Vegetable Crops, R.W.Michelmore University of California at Davis (UCD) Asmundson Hall, UCD, Davis, CA 95616, USA Tel: 1-(530)-742-1742 Fax: 1-(530)-752-9659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kozik,A., Michelmore,R.W., Knapp,S., Matvienko,M., Rieseberg,L.
Lin,H., van Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Elli
,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z.,
Church,S., Jackson,L. and Bradford,K.
Lettuce and Sunflower ESTs from the Compositae Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helianthus annuus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
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699 bp
QHG9D05.yg.abl QH_EFGHJ sunflower
clone QHG9D05, mRNA sequence.
BU027980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     http://compgenomics.ucdavis.edu/
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plate: QHG9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
belongs to contig QH_CA_Contig3066, see http://cgpdb.uc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Alexander Kozik [R.W.Michelmore]
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/cultivar="RHA280"
/db_xref="taxon:4232"
/clone="QHG9D05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    directionally cloned into a custom medium-copy vector and transformations made with four size classes to minimize size bias. Details of each source of RNA and library construction can be obtained at http://cgpdb.ucdavis.edu/TAG_LIB-OH_EFGHJ sunflower RHA280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Separate cDNAs were generated using primers that incorporated unique 5' and 3' tags to distinguish each source of RNA. cDNAs were then pooled, size-fractionated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /clone_lib="QH_EFGHJ sunflower RHA280"
/lab_host="E.coli"
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                                                                                                                                                                                                                                                                                                                                                                             Clemson University Genomics
Clemson University
100 Jordan Hall, Clemson, SC
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished (2001)
On Aug 14, 2000 this sequence version replaced
Contact: Wing RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Wei,F., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Oates,R. and Main,D.
Development of a genetically and physically anchored EST resource for barley genomics: Blumeria infected incompatible (Mla6) seedlift can be a seed of the companion of the compan
                                                                                                                                                                                                                                                                                                           Email: rwing@clemson.edu
Total hq bases = 569
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HV_CEB0023F16f Hordeum vulgare seedling green leaf EST library
HVCDNA0005 (Blumeria challenged) Hordeum vulgare cDNA clone
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hordeum vulgare
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BE559272
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                                                                                                                                                                                                                                                                            primer: AATTAACCCTCACTAAAGGG
                                                                                                                                                                                                           quality sequence stop: Location/Qualifiers
   /organism="Hordeum vulgare"
/Cultivar="CI16151 (Mla6)"
/db_xref="taxon:4513"
/Clone="HV_CEb0023F16f"
/clone_lib="Hordeum vulgare
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          vulgare
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CCTACCTAGGCTTCATCTACACATCCTTCCAAGAGAGAGCAACCTTCATATCCCATGCCA 742
                                                                                                                                                                                                                                     CTGGCGCAAGCCCAACTGCCTGGGCTGTTTGGACAAGAGCATGGACTGCTGAAGAAAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phred value 20 or above. For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley. To order this clone see http://www.genome.clemson.edu/orders Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)" a 194 c 184 g 187 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           at the Clemson University Genomics Institute (CUGI) (Begum Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates , Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: xhol; C.I. 16151 (Mla6) plants were greenhouse grown in the R Wise lab at Iowa State University, Ames, IA; 7 day old green seedlings were challenged with isolate 5874 (AVIMIa6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  library HVcDNA0005 (Blumeria challenged)"
/tissue_type="seedling green leaf"
/lab_host="SOLR"
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CCTACATGGGTTTCCTTTACACATCATTCCAAGAGAGAGCAACTTTCATATCCCATGGCA

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TATGATCACAGAAGAAGCACTTCCAACATATATGTCTATGCTCAATAGGTGTGATGGTAT
                                              GGAGTTGAGGGAAAGGGCCAAGGAGATTCCCGACGACTATTTTGTGGTGTTTAGTTGGAGA 431
                                                                                                          TTGGCAACCACAAGACTACTTGCCGGATCCGGTGTCAGACGGATTCGAGGAGCAAGTGCG 371
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                             TGCCAGCGCACTTGA 937
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                                                                                                                                                                                                                    459;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Japan Tel: 81-559-81-6856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hordeum vulgare subsp. vulgare.
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Er
Spermatophyta; Magnoliophyta; Liliopsida;
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EST.
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                                                                                                                                                                                                                   Conservative
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Location/Qualifiers
                                                                                                                                                                                                                                                                                        /clone_lib="K. Sato unpublished cDNA library, Mijo adult, heading stage top three leaves" /tissue_type="top three leaves" /dev_stage="adult, heading stage" | 146 c 165 g 162 t
                                                                                                                                                                                                                                                                                                                                                                                      /organism="Hordeum vulgare subsp. vulgare"
/cultivar="Haruna Nijo"
/db_xref="taxon:112509"
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73.6%;
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                                                                                                                                                                                                                                                                                                                                     University of Texas
Biology Building, Rov
Tel: 512 471 4238
Fax: 512 232 3402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cri2_8_L21_SP6 Ceratopteris Spore Library Ceratopteris richardii cDNA clone Cri2_8_L21 5', mRNA sequence.

BE643410
                                                                                                                                                                                                                                                                               Email: sroux@uts.cc.utexas.edu Plate: Cri2_8 row: L column: Seq primer: SP6.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Expressed sequence tags Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chatterjee, A., San Miguel, P., Stout, S.C., Expressed sequence tags of cDNA clones from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ceratopteris richardii
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EST.
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1 (bases 1 to 811)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae;
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                  250
                  Ø
              /cell_type="gpore"
/dev_stage="20 hours after germination initiation"
/dev_stage="20 hours after germination initiation"
/note="vector: pcMvspORT6; EST sequence from cDNA library
constructed from mRNA isolated from C.
richardii spores that had developed for 20 hours after
their germination had been initiated by white light."
150 c 201 g 207 t 3 others
                                                                                                                        /tissue_type="Gametophyte"
/cell_type="Gametophyte"
                                                                                                                                                                          /db_xref="taxon:49495"
/clone="Cri2_8_L21"
                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                               /cultivar="Brogn"
                                                                                                                                                                                                                               /organism="Ceratopteris richardii"
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                                                                AW509087 628 bp mRNA linear EST 03-DEC-2 si39h08.yl Gm-r1030 Glycine max cDNA clone GENOME SYSTEMS CLONE Gm-r1030-1336 5' similar to SW.STAD_SOYBN 042807 ACYL-[ACYL-CARR PROTEIN] DESATURASE PRECURSOR ; mRNA sequence.
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Pred. No. 4.9e-65;
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JOURNAL
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CAGACACGGTGATCTTCTTAACAAATATCTGTACTTGAGTGGACGAGTTGACATGAAACA
                         TAGACATGGTGACCTTCTCAATAAGTACCTTTATTTGTCTGGAAGGGTTGATATGAGGAA
                                                                                  AACAGGTGCCAGCCTTACTTCCTGGGCAATTTGGACAAGGGCATGGACTGCTGAAGAAAA
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4444 Forest Park Parkway, Box 85
Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Shoemaker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Public Soybean EST Project Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    digestion. The cDNA fragments were directionally cloned into the NotI-Sall restriction site of the psPoRT1 vector. The ligated cDNA fragments were transformed into E. coli ElectroMax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu Khanna. Note that Cm-r1030 is a re-rack of Gm-c1007."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             library construction kit. Complementary DNA was synthesized from mRNA using a poly(dT) sequence with a NotI restriction site. SalI linkers adapters were ligated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA library was constructed from mRNA isolated from immature cotyledons of greenhouse grown plants (individual seed fresh weight of 100-300mg). The 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS (
/clone_lib="Gm-r1030"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     was prepared using the Life Technologies pSuperScript cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pSPORT1; Site_1: SalI; Site_2: NotI; This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 355; DB 10;
Pred. No. 3.1e-64;
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9712 Medical Center Dr. Rockville, MD 20850,
Email: potato@tigr.org
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1 (bases 1 to 852)

Buell,C.R., Hart,A., Baker,B., Tanksley,S., Fry,W., Smart,C., Restrepo,S., Griffiths,H., van der Hoeven,R., Tsai,J. and
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This clone is available through the Research Genetics, contact
This clone is available through the Research Genetics for further information 1-800-711-6195 or
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On Jun 10, 2002 this sequence version
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Generation of a set of potato
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGTATCTGGGTTTTATCTACACTTCCTTCCAAGAGAGGGGCTACCTTCATTTCTCATGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTGAGAAGACTATTCAATATCTCATCGGCTCAGGAATGGATATCAAGTCAGAAAACAGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTGACTTTCTTCCTGATCCTGCCTCAGAAGGATTTGAAGACCAAGTCAAGGAGCTGCGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATGTTCAAGTTACTCATTCCATGCCGCCAGAGAGCGTGAAATCTTTGATTCCCTGCATG 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATACAGCTCGGCATGCTAAGGAGCATGGGGACATGAAACTAGCACAGGTATGTGGTATAA
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Expressed Sequence Tags f
Channel Inoculation with
Unpublished (2001)
Contact: Harris, Linda J.
                                                                                                                                                                     Harris,L.J., Balcerzak,M., Allard,S., Saparno,A., Moors,A., Hattori,J.I., Ouellet,T., Robert,L.S.,,D. and Tinker,N.A.
                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.

1 (bases 1 to 1055)
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BG837910
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73.1%;
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Pred. No. 6.6e-64;
0; Mismatches 171;
                                                                                                                              from Maize Silk Six Hours
                                                                                           Fusarium
                                                                                      graminearum
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Best Local Sim
Matches 496;
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                 AGGCGAGTGGAAGAAGTGCAGGGGAAGGAAGAAGAAAGCTGAGCACCCTGTT
                                                                        TTGGATTATTGCGACATCTTAGAGTTTCTGGTGGATAAATGGAATGTGGAAAGGCTTACG
                                                                                                                                                                                                 GACGACAACCTGTTCGAGCACTTCAGCGCGGTGGCGCAGAGGCTGGGCGTCTACACCGCC
                                                                                                                                                                                                                        GACGAACTTCTTTTAAACATTTCACGGCGGTTGCTCAGAGAGTGNGGGTTTATTCTGCG
                                                                                                                                                                                                                                                                           TTTGCTGACATGAGGAAGAAGATCACGATGCCAGCCCATCTCATGTACGACGGTAAG
                                                                                                                                                                                                                                                                                            TTTGCAGATATGATGCGCAAAAAAAATAACAATGCCAGCGCACTTGATGTACGACGGAAGT
                                                                                                                                                                                                                                                                                                                                               GCCTACACCAAGATAGTCGAGAAGCTCTTCGAGATGGACCCTGATTACACAGTGCTTGCG
                                                                                                                                                                                                                                                                                                                                                                  GCCTACACCAAGATCGTGGAAAAGCTCGCTGAGATCGACCCCGGACACAACAGTAATTGCT
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                                                   GGGCTGTCTGGAGAAGGGAGAAGGGCGCAGGACTTTGTCTGTACCTTGGCGCCGAGGATC
                                                                                                                           AAAGACTACGCCGACATCCTCGAGTTCCTGGTCCAGAGGTGGAAAGTCGCGGAGCTCACA
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CANADA
Tel: (613) 759-1314
Fax: (613) 759-6566
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="4-5 days post-silk emergence"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: EcoRI;
Site_2: XhoI, Field-grown corn was silk channel-inoculated
in the morning (-10 am) with 1 ml of a macroconidial
suspension (500,000 spores/ml) of Fusarium graminearum and
silk channels were collected and immediately frozen in
liquid nitrogen 6 hours later. RNA was extracted from
silk tissue between 1 cm below and above the inoculation
point in the silk channel, RNA from five silk channels was
pooled."
295 q 246 +
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     harrislj@em.agr.ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Zea mays"
/cultivar="C0388"
/db_xref="taxon:4577"
/clone="Zm10_10c08"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="Zm10_AAFC_ECORC_Fusarium_graminearum_corn_silk
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68.7%;
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Pred. No. 2.1e-63;
3; Mismatches 214;
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GACTGCTGAAGAAAACAGGCATGGTGATCTTCTGAACAAGTATATGTACCTTTCAGGACG
                                                         TGGTGTCCGAGATGAAACTGCCCAAGCCCAACTGCCTGGGCTGTTTGGACAAGAGCATG
                                                                                     TGGTATTAAGGATGAGACTGGGGCTGAGCCCAGTGCTTGGGCAATGTGGACTAGGGCATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Center For Genetic Resource Information National Institute of Genetics 1111 Yata, Mishima, Shizuoka 411-8540, Tel: 81-559-81-6855 Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barley EST sequencing project in Unpublished (2002)
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AV914373
AV914373.1 GI:18210150
EST.
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Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Em
Spermatophyta; Magnoliophyta; Liliopsida;
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/cultlvar="Haruna Nijo"
/db_xref="taxon:112509"
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/clone_lib="K. Sato unpublis
                                                                                                                                                                                                                                                                                                                                                                               /clone_lib="K. Sato unpublished
Nijo germination shoots"
/tissue_type="shoots"
/dev_stage="germination"
147 c 164 g 164 t
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Tel: 5
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BNICHLIF163 Six-day Cotton fiber Gossypium hirsutum cDNA 5' similar to ACYL-(ACYL-CARRIER PROTEIN) DESATURASE PRECURSOR (STERROYL-ACP DESATURASE) gi|508603 (L34346) stearcyl-acyl carrier protein desaturase (Glycine max), mRNA sequence.

AI730379.1 GI:5049231
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                                                                                                                                                                                                                                                                                                                                                          ESTs from developing Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
                                                                                                                                                                                                                                          Seq
                                                                                                                                                                                                                                                     Email: burr@bnlux1.bnl.gov
                                                                                                                                                                                                                                                                                                                              Biology Department
                                                                                                                                                                                                                                                                                                                                            Contact: Ben Burr
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516-344-3407
   Conservative
                                                                                                    /organism="Gossypium hirsutum"
/cultivar="Acala Maxxa"
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/tissue_type="immature fiber"
/dev_stage="5ix days post anthesis"
/lab_host="XL1-Blue"
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                                                                                                PROTEIN]
BE610498
                                                                                                           BE610498 606 bp mRNA linear EST 06-DEC-2001 607-1004 yl Gm-c1048 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1048-1448 5' similar to SW:STAD_SOYBN 042807 ACYL-[ACYL-CARRIER FROTEIN] DESATURASE PRECURSOR ;, mRNA sequence.
                                                                                    BE610498.1
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core eudicots;
ionoideae; Phaseoleae;
                             Tracheophyta;
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REFERENCE TITLE JOURNAL AUTHORS soybean.
Glycine max
Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tra
Spermatophyta; Magnoliophyta; eudicotyledons; core eudic
Spermatophyta; Magnoliophyta; Fabaceae; Papilionoideae;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., I Wylie, T., Underwood, K., Steptce, M., Theising, B., Allen, M., I Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., M., R., Waterston, R. and Wilson, R., Waterston, R. and Wilson, R., Public Soybean EST project 1 (bases 1 to 606) Shoemaker, R., Keim, P., V., A., Bolla, B., Marra, M.,

COMMENT

Contact: Shoemaker R/Public

Soybean

Project

., Bowers

Beck, C.,

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Public Soybean EST Project

Unpublished (1999)

clone

est@watson.wustl lone is available

edu through:

Invitrogen

2130

Washington University School of Medicine

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
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/dev_stage="1" week old"
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/note="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; The Clark NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from whole seedlings of 1 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a xhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). The library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."

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Sequence 17, Appl Sequence 17, Appl	Sequence 15, Appl Sequence 29, Appl	Sequence 15, Appl Sequence 15, Appl	Sequence 15, Appl	15	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 14, Appl	Sequence 14, Appl	Sequence 43, Appl

ALIGNMENTS

APPLICATION NUMBER: US/07/926,788A FILING DATE: 19920807 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: FILING DATE: FILING DATE: FILING DATE: ATTORNEY/AGENT INFORMATION: NAME: Ian C. McLeod REGISTRATION NUMBER: 20,931 REFERENCE/DOCKET NUMBER: MSU 4.1-156 TELECOMMUNICATION INFORMATION: TELEPHONE: (517) 347-4100 TELEFAX: (517) 347-4103 INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1309 Base Pairs TYPE: NUCLEIC ACID STRANDENMESS: Double TOPOLOGY: Linear MOLECULE TYPE: DESCRIPTION: CDNA HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:	WESULT 1 US-07-926-788A-1 SEQUENCE 1, Application US/07926788A PATENT NO. 5430134 GENERAL INFORMATION: APPLICANT: John B. Ohlrogge, Edgar B. APPLICANT: Cahoon, John Shanklin, APPLICANT: Choon, John Shanklin, TITLE OF INVENTION: A Method For TITLE OF INVENTION: Production of Petrogelinic Acid and 1 TITLE OF INVENTION: Hexadecanoic Acid in Transgenic Plants UMBER OF SEQUENCES: 1 CORRESSEE: Ian C. McLeod STREET: 2190 Commons Parkway CITY: Okemos STATE: Michigan COUNTRY: USA ZIP: 48864 COMPUTER READABLE FORM: MEDIUM TYPE: Storage COMPUTER: Acer OPERATING SYSTEM: MS-DOS (version 3.3) SOTTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
156	troselinic Acid d in Transgenic

Coriandrum sativum

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                                                                          GACGAGGGGCGAAAAGCGCAAGATATGTGTGTGTGTAATTGGGTCCCAAGATTAGGCGAGTG 1140
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                                                                                                                                                                                                                                                                                                                     AAGATCGTGGAAAAGCTCGCTGAGATCGACCCCGACACAACAGTAATTGCTTTTGCAGAT 900
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GAGGAGAAGGTTCAAGGCAAGG-----AGAAGAAAGCTGTGTTGCCTGTGGCTTTCAGC
                           GGTGAAGGGAGAAAGGCTCAAGAATATGTTTGTAGCTTGGCTGCTAAGATCAGGAGAGTT
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Pred. No. 6.6e-166;
0; Mismatches 222;
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                        TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 incl
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: MicrosoftWord 5.1 (a)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: L. STREET: Davis
CITY: Davis
CTATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Thompson, Gregory A
APPLICANT: Knauf, Vic C
TITLE OF INVENTION: Plant Desaturases Compositions
TITLE OF INVENTION: and Uses
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                                                                                                                                                                                                            TELEFONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEFAX: (916) 753-1510
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01746
FILING DATE: 14-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/762,762
FILING DATE: 16-SEPT-1991
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                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 16-MAR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                      NAME: Lassen, Elizabeth REGISTRATION NUMBER: 31, NAME: Donna E Scherer REGISTRATION NUMBER: 34
                                                                                                                                                                                                                                                                                      NAME: Carl J. Schwedler REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Calgene, Inc. STREET: 1920 Fifth Street
                                                                                         TOPOLOGY:
                                                                                                         STRANDEDNESS:
                                                                                                                            TYPE:
                                                                                                                                           LENGTH: 1668 base pairs
                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/494,106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TGGATTTTCAATCGGGAGTTGAAGATATGA 1230
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Score 572; DB 1;
Pred. No. 5.4e-154;
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Matches 823;

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                                                                                                  GAAGGTGGATAAACTAACGGGCCTTTCAGCTGAGGGGACAAAAGGCTCAGGACTATGTTTG
                                                                                                                    GAATGTGGAAAAGGCTTACGGGGCTGTCGGACGACGAGGGCCGAAAAAGCGCAGGAATATGTGTG
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                                                TGAATTGGGTCCCAAGATTAGGCGAGTGGAAGAAGAGTGCAGGGGAAGGAGAAGAAGAA
                                                                                                                                                                    TCTTGGAGTCTACACAGCAAAGGATTATGCAGATATTTGGAGTTCTTGGTGGGCAGATG
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RESULT 3
US-08-926-522-3
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                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: 08/4:
FILING DATE: 2-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Vic C. Knauf
APPLICANT: Gregory A. Thompson
TITLE OF INVENTION: PLANT SEED OILS
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 31,8
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,7
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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CITY: Davis
STATE: CA
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                                                                                                                                                                                                          111 ACCAGTGACCAGAGTTAGCTCTCCAAGGGTTTTCATGGCTTCCACTGTCAACTCTAACTC 170
   273
                                     209
                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (910) 753-1510 TO NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh 7.1 SOFTWARE: Microsoft Word 5.1(a)
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                                                                                                                                                                           89
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                                                  CACTCACTCTATGCCACCCCAAAAGCTAGAAATATTCAAGTCCCTTGATGATTGGGCTAG
                                                                                                        TAAGGAAGTTGAGAATCTCAAGAAGCCTTTTCATGCCTCCTCGGGAGGTACATGTTCAGGT
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                                     TACCCATTCTATGCCACCCCAAAAGATTGAGATCTTTAAATCCCTAGACAATTGGGCTGA
                                                                                                                                       CATGGTTCTTGATAATCTCAAAAGTCC------
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                                                                                                                                                                                                                                            Score 572; DB 4;
Pred. No. 5.4e-154;
0; Mismatches 341;
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RESULT 4
PCT-US91-01746-15
; Sequence 15, Application PC/TUS9101746
; GENERAL INFORMATION:
; APPLICANT: Thompson, Gregory A
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                                                                                                AGGAAGGGAAGGGAGTGAGGAGTGAGTAGTAGATTTTCTATATGC
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                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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TITLE OF INVENTION: P
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CITY: L
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NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE,DOCKET NUMBER: CGNE
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEPAX: (916) 753-1510
TELEPAX: (916) 753-1510
TELEPAX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: Apple Macintosh OPERATING SYSTEM: Macintosh SOFTWARE: Microsoftword 4.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31, 8
NAME: Donna E. Scherer
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 1: MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                             ACCAGTGACCAGAGTTAGCTCTCCAAGGGTTTTCATGGCTTCCACTGTCAACTCTAACTC
                                                     GCCGGATCCGGTGTCAGACGGATTCGAGGAAGCAAGTGCGGGAGTTGAGGGAAAGGGCCAA 392
                                                                                                                                                                                   CACTCACTCTATGCCACCCCAAAAGCTAGAAATATTCAAGTCCCTTGATGATTGGGCTAG
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GAACAATGTGTTGATTCACCTCAAATCTGTCGAGAAATCTTTGGCAACCACAAGACTACTT
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Plant Desaturases-Compositions and
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                                                                                                                                                                                                                                                                                                                                          Score 572; DB 5;
Pred. No. 5.4e-154;
0; Mismatches 341;
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RESULT 5
US-07-721-761A-32
                                                                                                                               Sequence 32, Application US/07721761A Patent No. 5475099
GENERAL INFORMATION:
                                              APPLICANT: Vic. C. Knauf
APPLICANT: Gregory A. Thompson
TITLE OF INVENTION: Plant Fatty Acid
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
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STREET: 1920
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
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                                                                                                                                                                                                                                                                           GAAAGCTGAGCACCCTGTTTCTTTCAGCTGGATTTTCAATCGGGAGTTGAAGATATGAAC 1232
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; TYPE: NUCLEIC ACID
; STRANDEDNESS: sing,
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA 1
US-07-721-761A-32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (916) 753-15 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (916) 753-6313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/568,493
FILING DATE: 15-AUGUST-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 19910620
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Donna E. Scherer REGISTRATION NUMBER: 34. REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                   ATCGGCTCAGGAATGGATATCAAGTCAGAAAACAGCCCCTACCCTAGGCTTCATCTACACA
                                                                                                                                                                        TACCTTTATTTGTCTGGAAGGGTTGATATGAGAAAATTGAGAAGACTATTCAATATCTC
                                                                                                                                                                                                                                               GCAATGTGGACTAGGGCATGGACTGCCGAAGAGAATAGACATGGTGACCTTCTCAATAAG
                                                                                                                                                                                                                                                                                                    ACAATGCTTAATACCCTAGATGGTGTACGTGATGAGACTGGGGCTAGCCTTACGCCTTGG
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 TCGTTTCAAGAGCGTGCCACATTTGTTTCTCACGGAAACACCGCCAGGCATGCAAAGGAT
                                                                          ATTGGGTCAGGAATGGATCCTCGTACCGAAAACAGCCCCTACCTTGGGTTCATCTACACA
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Pred. No. 1.1e-139;
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US-07-978-687-32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Patent No. 5510255
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                    SOFTWARE: MICROSOFT WORD 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/978
FILING DATE: FEBRUARY 1, 199:
                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintos
                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 15-AUGU
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Vic. C. Knauf
APPLICANT: Gregory A. Thompson
TITLE OF INVENTION: Plant Fatt;
NUMBER OF SEQUENCES: 51
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                                                        ATTORNEY/AGENT INFORMATION:
                                                                                                  PRIOR APPLICATION DATA:
                                                                                                                                                                                       PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: C
STREET: 1920
CITY: Davis
STATE: CA
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                                                                                                                                                            APPLICATION NUMBER: FILING DATE: 15-AUG
                                                                        FILING DATE:
                                                                                                                                                                                                      CLASSIFICATION:
                              REGISTRATION NUMBER:
                                            NAME:
                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
 REGISTRATION
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No. 5510255
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                                             Elizabeth
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                                                                                                                                                                                                                                                                                                                                                                                              E: Calgene, Inc.
1920 Fifth Street
                                                                                                                                                                                                                                                                                                                                                       USA
E. Scherer
NUMBER: 3
                                                                                                                                                            15-AUGUST-1991
                                                                                                                   15-AUGUST-1990
                                                                                                                                                                                                                    FEBRUARY 1, 1993
                                                                        26-JUNE-1991
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                                         Lassen
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US-07-978-687-32
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TELECOMMUNICATION INFORMATION:
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LENGTH: 1533 base pairs
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                                                               ATTGCTTTTGCAGATATGATGCGCAAAAAAAATAACAATGCCAGCGCACTTGATGTACGAC
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GGGCGTGATGACAACCTCTTCGAACATTTCTCGGCGGTTGCCCAAAGACTCGGCGTCTAC
                                                                                                     GCCACAGCCTACACCAAGATCGTGGAAAAGCTCGCTGAGATCGACCCCGACACAACAGTA
                                                                                                                                                          CATGGGGACGTGAAACTGGCGCAAATTTGTGGTACAATCGCGTCTGACGAAAAGCGTCAC
                                                                                                                                                                                   TACGGCGACAAGAACCTCGCTCACATCTGCGGCTCCATCGCCTCCGACGAGAAGCGCCAC
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Pred. No. 1.1e-139;
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INFORMATION FOR SEQ
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                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/762
FILING DATE: 16-SEPT-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/USS
FILING DATE: 14-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Plant Desaturases-Compositions TITLE OF INVENTION: and Uses NUMBER OF SEQUENCES: 45
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                                       NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: (
FILING DATE: 13-AUG-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Thompson, (APPLICANT: Knauf, Vic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1201
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                                                                                                                                                                                    FILING DATE: 16-MAR-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
                                                                                                                                                       NAME: Lassen, Elizabeth REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/615,784 FILING DATE: 14-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM:
SOFTWARE: Microsc
                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 6-JUNE-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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                                                                                                                         REGISTRATION NUMBER:
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1920 Fifth Street
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ID NO:
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Best Local 9
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LENGTH: 1533 base pairs
TYPE: nucleic acid
STRANDENESS: double
TOPOLOGY: linear
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                                                                             CATGGGGACGTGAAACTGGCGCAAATTTGTGGTACAATCGCGTCTGACGAAAAGCGTCAC
                                                                                                                                                                                                                                                             TACGGCGACAAGAACCTCGCTCACATCTGCGGCTCCATCGCCTCCGACGAGAAGCGCCAC
                                                                                                                                                                                                                                                                                                                                                                                  ACAATGCTTAATACCCTAGATGGTGTACGTGATGAGACTGGGGCTAGCCTTACGCCTTGG
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TCTGCGTTGGATTATTGCGACATCTTAGAGTTTTCTGGTGGATAAATGGAATGTGGAAAGG
                                                                                                                                    CTTGCTTTTGCCGACATGATGAGGAAAAAGATCTCGATGCCCGCACACTTGATGTACGAT 1020
                                                                                                                                                  ATTGCTTTTGCAGATATGATGCGCAAAAAAATAACAATGCCAGCGCACTTGATGTACGAC
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                                                                                                                                                                                          GCCACAGCCTACACCAAGATCGTGGAAAAGCTCGCTGAGATCGACCCCGACACAACAGTA 885
                                                                                                                                                                                                                                                                                                     TCGTTTCAAGAGCGTGCCACATTTGTTTCTCACGGAAACACCGCCAGGCATGCAAAGGAT
                                                                                                                                                                                                                                                                                                                  ATTGGGTCAGGAATGGATCCTCGTACCGAAAACAGCCCCTACCTTGGGTTCATCTACACA
                                                                                                                                                                                                                                                                                                                                                                                                               TATCTCTACCTTTCTGGGCGGGTAGACATGAGGCAGATACAGAAGACAATTCAGTATCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCTGAAGGATTTGATGAACAAGTCAAGGAACTAAGGGCAAGAGCAAAGGAGATTCCTGAT
                           ACCGCCAAAGACTACGCCGACATACTGGAATTTCTGGTCGGGCGGTGGAAAGTGGCGGAT 1140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity
739; Conserv
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68.5%;
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Pred. No 1.1e-139;
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US-08-926-522-1
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Best Local :
                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,173
FILING DATE: 2-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: VIC C. Knauf
APPLICANT: Gregory A. Thompson
TITLE OF INVENTION: PLANT SEED OILS
                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (916) 753-151
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1(a)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,522
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
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                                                                                                      241 AATGCCAAGAAGCCTTTTCAACCTCCACGAGAGGTTCATGTTCAGGTGACGCACTCCATG
                                                                                                                                     NAME: Donna E. Scherer
REGISTRATION NUMBER: 34
NAME: Carl J. Schwedler
                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
STRANDEDNESS: double
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CITY: Davis
                                                                                                                                                                       7 Match 38.8%; Score 522; DB 4; Length 15 Local Similarity 68.5%; Pred. No. 1.1e-139; Nes 739; Conservative 0; Mismatches 331; Indels
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ZIP: 95616
                                                                                                                                                                                                                                                                                                                                  LENGTH:
ATTCACCTCAAATCTGTCGAGAAATCTTGGCCAACCACAAGACTACTTGCCGGATCCGGTG 345
                                    CCACCACAGAAGATAGAGATTTTCAAATCCATCGAGGGTTGGGCTGAGCAGAACATATTG
                                                    CCACCCCAAAAGCTAGAAATATTCAAGTCCCTTGATGATTGGGCTAGGAACAATGTGTTG
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                                                                                                                                                                       Gaps
                                  360
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310	GTTGTTCCATTCAGCTGGATTTTCGATAGACAGGTGAAGCTGTGAAGAAAAAAAA	1252	ф
244	CCTGTTTCTTCAGCTGGATTTTCAATCGGGAGTTGAAGATATGAACAGGAAGGGAAGG 1:		ν
1251	AGAATCAGAAGGCTGGAGGAGAGGCTCAAGGGCGAGCAAAGGAAGGACCT	1201	В
1185	ANGATTAGGCGAGTGGAAGAAAAGTGCAGGGGAAGGAAGAAGAAGAAGAAGAAGCAC	1126	Ωy
1125 1200	066 CTTACGGGGCTGTCGGACGAGGGGGCGAAAAGCGCAGGAATATGTGTGTG	1066 1141	8 8
	ACCGCCAAAGACTACGCCGACATACTGGAATTTCTGGTCGGGCGGTGGAAAGTGGCGGAT	1081	₽
1065	TCTGCGTTGGATTATTGCGACATCTTAGAGTTTTCTGGTGGATAAATGGAATGTGGAAAGG	1006	Qγ
1080	GGCGTGATGACAACCTCTTCGAACATTTCTCGGCGGTTGCCCAAAGACTCGGCGGTCTAC	1021	В
	GGAAGTGACGAACTTCTTTTAAACATTTCACGGCGGTTGCTCAGAGAGTGNGGGTTTAT	946	ΩY
1020	THE CTTGCTTTTGCCGACATGATGATGAGGAAAAAGATCTCGATGCCCGCACACTTGATGTAACGAT	961	8 8
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825	TACGGCGACAAGAACCTCGCTCACATCTGCGGCTCCATCGCCTCCGACGAGGAGAAGCGCCAC	766	2 8
840	TCGTTTCAAGAGCGTGCCACATTTGTTTCTCACGGAAACACCGCCAGGCATGCAAAGGAT	781	В
765	TCCTTCCAAGAGAGGAGCAACCTTCATATCCCATGCCAACACAGGCCAAGCAGGCCAAGCTGGCCCAACAC	706	ΩУ
780	ATTGGGTCAGGAATGGATCCTCGTACCGAAAACAGCCCCTACCTTGGGTTCATCTACACA	721	Вb
705	ATCGGCTCAGGAATGGATATCAAGTCAGAAAACAGCCCCTACCTA	646	ΩУ
720		661	Вb
645	TACCTTTATTTGTCTGGAAGGGTTGATATGAGGAAAATTGAGAAGACTATTCAATATCTC	586	VQ
660	GCTGTCTGGACTAGGGCTTGGACAGCTGAAGAGAACAGGCATGGCGATCTTCTCCACACC	601	B
585	GCAATGTGGACTAGGGCATGGACTGCCGAAGAGAATAGACATGGTGACCTTCTCAATAAG	526	Ϋ́
600	ACAATGCTTAATACCCTAGATGGTGTACGTGATGAGACTGGGGCTAGCCTTACGCCTTGG	541	В
525	TCTATGCTCAATAGGTGTGATGGTATTAAGGATGAGACTGGGGCTGAGCCCAGTGCTTGG	466	Qγ
540	GATTACTTTGTTTTTGGTTGGÅGATATGATTACAGAGGAAGCCCTACCTACCTACCAA	481	В
465	GACTATTTTGTGGTGTTAGTTGGAGATATGATCACAGAAGAAGCACTTCCAACATATATG	406	QУ
480	TCTGAAGGATTTGATGAACAAGTCAAGGAACTAAGGGCAAGAGCAAAGGAGATTCCTGAT	421	В
405	TCAGACGGATTCGAGGAGCAAGTGCGGGAGTTGAGGGAAAGGGCCCAAGGAGATTCCCGAC	346	Ωy
420	GTTCACCTAAAGCCAGTGGAGAAATGTTGGCAAGCACAGGATTTCTTGCCGGACCCTGCA	361	Ъ

PCT-US91-01746-12
; Sequence 12, Application PC/TUS9101746
; GENERAL INFORMATION:

APPLICANT: Thompson, Gregory A
APPLICANT: Knauf, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions and Uses
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

RESULT

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TELEX: 350370 CGNE
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
FENGTH: 1533 base pairs
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Best Local S
Matches 739
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/615,784
FILING DATE: 14-NOV-1990
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
APPLICATION NUMBER: 07/494,106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION UMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
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STREET: 19
CITY: Davi
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wes 739; Conserv
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STRANDEDNESS:
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                                                                         TCTATGCTCAATAGGTGTGATGGTATTAAGGATGAGACTGGGGCTGAGCCCAGTGCTTGG
                                                                                                                                                                             TCTGAAGGATTTGATGAACAAGTCAAGGAACTAAGGGCAAGAGCAAAGGAGATTCCTGAT 480
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GCTGTCTGGACTAGGGCTTGGACAGCTGAAGAGAACAGGCATGGCGATCTTCTCCACACC
                                                         ACAATGCTTAATACCCTAGATGGTGTACGTGATGAGACTGGGGGTAGCCTTACGCCTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 522; DB 5; Le
Pred. No. 1.1e-139;
0; Mismatches 331;
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660
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RESULT 10
PCT-US91-05801-32
; Sequence 32, Application PC/TUS9105801
; GENERAL INFORMATION:
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                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 i
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh (
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
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ADDRESSEE: Calgene,
                                                                                                                                                                                                                                                                                                                                   APPLICANT: Vic. C. Knauf APPLICANT: Gregory A. Th
                                         CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                             COUNTRY: 21P: 956
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CITY: E
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           APPLICATION NUMBER: 07/568, FILING DATE: 15-AUGUST-1990
                                                                       APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                            STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCTGTTTCTTTCAGCTGGATTTTCAATCGGGAGTTGAAGATATGAACAGGAAGGGAAGG 1244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTGCTTTTTGCAGATATGATGCGCAAAAAAAATAACAATGCCAGCGCACTTGATGTACGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACCTTTATTTGTCTGGAAGGGTTGATATGAGGAAAATTGAGAAGACTATTCĀĀTATCTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AGAATCAGAAGGCTGGAGGAGAGAGCTCAAGGGCGAGCAAAG-----GAAGGACCT 1251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTGACCGGCCTATCTGGTGAAGGGCGTAAAGCGCAAGATTATGTTTGCGGGGTTGCCACCA 1200
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                                                                                                                                                                                                  95616
                                                                                                                                                                                                                                            Davis
                                                                                                                                                                                                                                                        E: Calgene, Inc.
1920 Fifth Street
                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                     Plant Fatty Acid
                                                                                                                                                                                                                                                                                                                                   Thompson
                                                                                       PCT/US91/05801
                                                                                                                                                                 3.50 inch,
                                                                                                                                    6.0.7
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PCT-US91-05801-32
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Best Local Sim
Matches 739;
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFORMUNICATION INFORMATION:
TELEFAX: (916) 753-6313
TELEFAX: (916) 753-1510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 07/72
FILING DATE: 26-JUNE-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: 11 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Elizabeth Lassen REGISTRATION NUMBER: 31,845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
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                                                                                                                                                                                                                      CATGGGGACGTGAAACTGGCGCAAATTTGTGGTACAATCGCGTCTGACGAAAAGCGTCAC
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ATTGCTTTTGCAGATATGATGCGCAAAAAAATAACAATGCCAGCGCACTTGATGTACGAC
                             GCCACAGCCTACACCAAGATCGTGGAAAAAGCTCGCTGAGATCGACCCCGACACACAGTA
                                                                                                           TACGGCGACAAGAACCTCGCTCACATCTGCGGCTCCATCGCCTCCGACGAGAAGCGCCAC
                                                                                                                                                                        TCCTTCCAAGAGAGAGCAACCTTCATATCCCAATGCCAACACACAGCCAAGCTGGCCCAACAC
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ER: CGNE
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Pred. No. 1.1e-139;
0; Mismatches 331;
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US-07-995-657-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                    TELEX: 835420
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1201
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                                                                                                                                                                                                                                              APPLICATION NUMBER: US/07/995,65
FILING DATE: 19921211
FILING DATE: C) CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1252
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          MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1066
                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 302-892-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
HYPOTHETICAL:
                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           961
                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 1007 Mark CITY: Wilmington STATE: Delaware COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              946
                                                                                                                                                                                                                                                                                                                                   COMPUTER: Macintosh
OPERATING SYSTEM: Ma
SOFTWARE: Microsoft
                                                                                                                                                                         REFERENCE/DOCKET NUMBER: BB.
                                                                                                                                                                                       NAME: GEIGER, KATHLI
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                            TOPOLOGY:
                                          STRANDEDNESS: single
                                                                       LENGTH:
                                                                                                                                TELEFAX:
                                                                                                                                                                                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1007 Market Street
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                                                                     2243 base pairs
                                                                                                                                  302-892-7949
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Yadav, Narendra S.
                            linear
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   NO
               cDNA to mRNA
                                                                                                                                                                                                   KATHLEEN W.
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NAME/KEY: 3' non-coding sequence
LOCATION: 1246..2243
COTHER INFORMATION: /note= "IDENTIFICATION"
OTHER INFORMATION: MCTHOD=Established by proximity to location;
OTHER INFORMATION: 1243-1245"
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Best Local Similarity
Matches 743; Conserv
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OTHER INFORMATION: pu
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LIBRARY: CDNA
                        394
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                                                                                                                                                                           274 AACAATGTGTTGATTCACCTCAAATCTGTCGAGAAATCTTGGCAACCACAAGACTACTTG 333
                                                                                                                                                                                                                         238
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                                                                                                                                                                                                                                                                                                                                                                              118 CAAATGCCCAGCCTCAGATCTCCCCCGCTTCCGCATGGCTTCCACCCTCCGGCTCCGGTTCC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Putative transit peptide coding sequence LOCATION: 70..165
OTHER INFORMATION: /note= "IDENTIFICATION OTHER INFORMATION: METHOD-Deduced by proximity to OTHER INFORMATION: and location 166-1242"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: Translation termination codon LOCATION: 1243..1245
OTHER INFORMATION: METHOD-The translatic OTHER INFORMATION: reading frame for a COTHER INFORMATION: size"
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OTHER INFORMATION: /note= "IDENTIFICATION OTHER INFORMATION: METHOD-Similarity of the cont OTHER INFORMATION: methionine codon in the open OTHER INFORMATION: translation
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OTHER INFORMATION:
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STRAIN: Cultivar Wye
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GAGATTCCCGACGACTATTTTGTGGTGTTAGTTGGAGATATGATCACAGAAGAAGCACTT
                                                                                                                                      CAGAACATCTTGACTCATCTTAAACCTGTAGAAAATGTTGGCAACCACAGGATTTTTTA 357
                                                                                                                                                                                                                   ACTCACTCTATGCCACCCCAAAAGCTAGAAATATTCAAGTCCCTTGATGATTGGGCTAGG 273
                                                                              CCGGATCCGGTGTCAGACGGATTCGAGGAGCAAGTGCGGGAGTTGAGGGAAAGGGCCAAG 393
                                                         AAAGAGGTTGAAAATATTAAGAAGCCATTCACTCCTCCCAGAGAAGTGCATGTTCAAGTA 237
                                                                                                                                                                                                                                                                                                                                      ATGGTTCTTGATAATCTCAAAAGTCCGCCAA-------ATCTTCAAGTC 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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METHOD=The translation codon ends the open
reading frame for a protein of the expected
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METHOD=Similarity of the context of the
methionine codon in the open reading frame to
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 521.2; DB 1;
Pred. No. 2.2e-139;
0; Mismatches 324;
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ACATATACAGATGATTACTTTGTTGTTCAACAATAAGATGATTACTTATCAAATAAGTGTCTATGCTAACTAA	TACTTTGTTGTT TACTTTGTTGTT ATGCTCAATAGG ATGCTCAATAGG ATGTTAAATACT ATGTTAAATACT ATGTGACTAGG ATTTTGGACTAGG ATTTTGGACTAGG ATTTTGGACTAGG ATTTTGACAAGAGATG [RESULT 12 US-08-474-587-1 ; Sequence 1, Appl ; Patent No. 57602 ; GENERAL INFORMA ; APPLICANT: H APPLICANT: Y APPLICANT: Y APPLICANT: Y ITILE OF INVE ; Patent No. 57602 ; Patent OF INVE ; TITLE OF INVE ; TITLE OF INVE ; ORRESPONDENC ADDRESSEE: ADDRESSEE:	1198	Qy 1174 AAAGC	1114	Qy 1054 AATGT Db 1078 AAGGT	Qy 994 GTGNG Db 1018 ATTGG	Qy 934 TTGAT Db 958 CTTAT	Qy 874 GACAC Db 898 GATGG	Qy 814 GAGAA Db 838 GAGAA	Qy 754 CTGGC 	Qy 694 TTCAT Db 718 TTCAT	Qy 634 ATTCA Db 658 ATTCA	Qy 574 CTTCT Db 598 CTTCT	Qy 514 CCCAG pb 538 CTTAC	QY 454 CCAAC Db 478 CCTAC	Db 418 GAGAT
	TGTCGGAGACATGATCACAGAGGAAA TGATGGTATTAAGGATGAGACTGGGG GATGGACTGCGAAGAGAAAAAAAAAA	ication US/08474587 06 07 100: 11c, William D. adav, Marendra S. erez_Grau, Luis NTION: Nucleotide S 06 06 08 NTION: Soybean Stea NTION: Desaturase c UENCES: 12 E. I. du Pont de Ne and Company	120	GCCACCAAGAATCAGAAGGTTGGA	GGGTCCCAAGATTAGGCGAGTGGA	GGAAAGGCTTACGGGGCTGTCGGA 	GGTTTATTCTGCGTTGGATTATTG	GTACGACGGAAGTGACGAACTTCT 	AACAGTAATTGCTTTTGCAGATAT	.GCGCCACGCCACAGCCTACACCAA 	CCAACACTACGGCGACAAGAACCT	CTACACATCCTTCCAAGAGAGAGGC	ATATCTCATCGGCTCAGGAATGGA GTACCTTATTGGGTCTGGGATGGA	CAATAAGTACCTTTATTTGTCTGG 	TGCTTGGGCAATGTGGACTAGGGC 	ATATATGTCTATGCTCAATAGGTG	TCCAGATGATTACTTTGTTGTTCT

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TELEX: 835420
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 30,684
REFERENCE/DOCKET NUMBER: BB_1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 302-992-4931
TELEFAX: 302-773-0164
                                                                                                                                                                                                                                                                                                                                         FEATURE: Putative t
NAME/EN: Putative t
LOCATION: 70..165
OTHER INFORMATION: /
OTHER INFORMATION: M
OTHER INFORMATION: L
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LIBRARY: cDNA t
CLONE: pDS1
FEATURE:
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LOCATION: 166..1242
OTHER INFORMATION: ME
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APPLICATION NUMBER:
FILING DATE:
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                      NAME/REY: Translation termination codon LOCATION: 1243.1245
OTHER INFORMATION: /note= "IDENTIFICATION" (THE INFORMATION: METHOD=The translation codon ends the open in the property of the codon ends the open in the codon ends 
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OTHER INFORMATION: /note- "IDENT: OTHER INFORMATION: METHOD=Deducee OTHER INFORMATION: to location 7/
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TOPOLOGY: li
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SOFTWARE: Microsc
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Microsoft Word, 4.
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METHOD=The translation codon ends the open reading frame for a protein of the
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; FEATURE:
; NAME/KEY: 3' non-co
; LOCATION: 1246..224
; OTHER INFORMATION:
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Best Local
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                                                                                                     GAGAAGCGCCACGCCACAGCCTACACCAAGATCGTGGAAAAGCTCGCTGAGATCGACCCC
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                                       TTGATGTACGACGGAAGTGACGAACTTCTTTTTAAACATTTCACGGCGGTTGCTCAGAGA 993
                                                                                 GATGGTACAGTTATGGCATTTGCCGACATGATGAGGAAGAAGATTGCTATGCCAGCACAC
                                                                                                                                                                     GAGAAGCGCCACGAGACTGCATACACAAAGATAGTGGAAAAGCTGTTTGAGGTTGATCCT
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Pred. No. 2.2e-139;
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US-08-679-645-1
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                                                                                                                                                                     CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/
FILING DATE: July 12, 1996
CLASSIFICATION: 800
PRIOR APPLICATION: BOTA:
APPLICATION NUMBER: 60/001
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300
FILING DATE: July 13, 1995
APPLICATION NUMBER: 08/300
FILING DATE: September 2,
ATTORNEY/AGENT INFORMATION:
NAME: WAIDLUTG, Richard J.
REGISTRATION NUMBER: 32,32
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                                                                           INFORMATION FOR SEQ ID NO: 1:
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APPLICANT:
APPLICANT:
                         SEQUENCE CHARACTERISTICS:
LENGTH: 1621 base pairs
TYPE: nucleic acid
                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: IBM P.C. SOFTWARE: Word Perfect 5.1
TOPOLOGY: 11
                                                                                                                                                       REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 219/247
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Merlo, Donald J.
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Matches 687; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      192 AAGTCCGCCAAATCTTCAAGTCACTCACTCTATGCCACCCCAAAAGCCTAGAAATATTCAA 251
                                                                                    TTTCACGGCGGTTGCTCAGAGAGTGNGGGTTTATTCTGCGTTTGGATTATTGCGACATCTT 1031
                                                                                                                                                                                                                  AAAAATAACAATGCCAGCGCACTTGATGTACGACGGAAGTGACGAACTTCTTTTTAAACA
                                                                                                                                                                                                                                                                             AAAGCTCGCTGAGATCGACCCCGACACAGTAATTGCTTTTTGCAGATATGATGCGCAA
                                                                                                                                                                                                                                                                                                                                    TGAGGAGAACAGGCATGGTGATCTGCTCAACAAGTATATGTACCTCACTGGGAGGGTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTCCCTTGATGATTGGGCTAGGAACAATGTGTTGATTCACCTCAAATCTGTCGAGAAATC 311
GCAGGGGAAGGAGAA
                            CAAGGCGCAGGACTACCTTTGCACCCTTGCTTCAAGAATCAGGAGGCTGGAGGAGAGGGC
                                                AAAAGCGCAGGAATATGTGTGTGAATTGGGTCCCAAGATTAGGCGAGTGGAAGAAAAGT
                                                                                                                AGAGTTTCTGGTGGATAAATGGAATGTGGAAAGGCTTACGGGGGCTGTCGGACGAGGGGCG 1091
                                                                                                                                             CTTCTCCATGGTCGCGCAGAGGCTTGGCGTTTACACCGCCAGGGACTACGCCGACATCCT
                                                                                                                                                                                                      GAAGATCTCAATGCCTGCCCACCTGATGTTTGACGGGCAGGACGACGACGATGTTCGAGCA
                                                                                                                                                                                                                                                            GAAGCTGTTTGAGATCGACCCTGATGGTACCGTGGTCGCTCTGGCTGACATGATGAGGAA 1017
                                                                                                                                                                                                                                                                                                                     CTGCGGCATCATCGCCTCAGATGAGAAGCGACATGAAACTGCGTACACCAAGATCGTGGA
                                                                                                                                                                                                                                                                                                                                                                              CTCACACGGGAACACTGCTCGTCACGCCAAGGACTTTGGCGACTTAAAGCTTTGCACAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGAGATGAGACAGGTGCAAGCCCCACTGCCTGGGCTGTTTGGACGAGGGCATGGACTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTCGCTTGATGATTGGGCTAGAGATAATATCTTGACGCATCTCAAGCCAGTCGAGAAGTG
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Pred. No. 4.2e-137;
O; Mismatches 291;
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1258 CCAGAGCAGAGCCAAGAA 1275

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; TOPOLOGY: 1i; MOLECULE TYPE: US-08-471-791-19
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US-08-471-791-19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 19, Application US/08471791
Patent No. 5723595
GENERAL INFORMATION:
APPLICANT: Thompson, Gregory A
APPLICANT: Knauf, Vic C
TITLE OF INVENTION: Plant Desaturases-Compositions
TITLE OF INVENTION: and Uses
    Query Match
Best Local Similarity
Matches 715; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 07/762,762
FILING DATE: 16-SEPT-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/01746
FILING DATE: 14-MAR-1991
CLASSIFICATION ATA:
APPLICATION ATA:
APPLICATION UMBER: 07/615,784
PRIOR APPLICATION NUMBER: 07/615,784
APPLICATION NUMBER: 07/615,784
APPLICATION NUMBER: 07/615,784
PRIOR APPLICATION NUMBER: 07/615,784
                                                                                                                                                         INFORMATION FOR SEQ ID NO: 19: SEQUENCE CHARACTERISTICS: LENGTH: 1495 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintos
                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: CG
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/494,:
FILING DATE: 16-MAR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Lassen, Elizabeth
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/567,373
FILING DATE: 13-AUG-1990
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: MicrosoftWord 5.1 (a) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
                                                                                                                                                                                                                               TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
TELEX: 350370 CGNE
                                                                                                                                                                                                                                                                                                                                         NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 6-JUNE
                                                                                                                                          STRANDEDNESS:
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      Conservative
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                                                                                                   cDNA to mRNA
                                                                                                                                          double
                    38.1%;
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  Score 511.8; DB 1; Pred. No. 8.8e-137; 0; Mismatches 308;
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	TATGAACAGGAA 1237	1226	Qу
1261	AGAAAGGACCCAAGGTTCCTTTCAGCTGGATACATGACAGAGAAGTGCAGC	1211	Db
1225		1166	Qy
1210		1151	Db
1165	ATGTGTGTGAATTTGGGTCCCAAGATTAGGCGAGTGGAAGAAGAGAAGTGCAGGGGGAAGGAGA	1106	Qy
1150	AAGAGT	1091	Db
1105	ATAAATGGAATGTGGAAAAGGCTTACGGGCCTGTCGGACGAGGGGCGAAAAGCCCCAGGAAT	1046	Qy
1090	GCTCGGTGTTTACACTGCCAAAGACTATGCGGACATTCTTGAGTTTTTGGTTG	1031	Db
1045	TCTGCGTTGGATTATTGCGACATCTTAGAGTTTCTGGTGG	986	Qy
1030	ACTTCTCTTCTGTTG	971	Db
985		926	Qy
970	TGATGGTACTGTGATGGCGTTTGCAGACATGATGAGGAAGAAATCTCGATGC	911	Db
925	CCGACACAACAGTAATTGCTTTTGCAGATATGATGCGCAAAAAAAA	866	Qy
910		851	Db
865	CCTCCGACGAGAAGCGCCACGCCCACAGCCTACACATCGTGGAAAAGCTCGCTGAGA	806	Qy
850	CAGCTCGCCAAGCCAAAGAGCACGGAGACCTCAAGCTAGCCCAAATCTGCGGCACAATAG	791	Db
805	AGCCAAGCTGGCCCAACACTACGGCGACAAGAACCTCGCTCACATCTGCGGCTCCATCG	746	Qy
790	ACCTCGGCTTCATCTACACTTCATTCCAAGAAAGAGCCACCTTCATCTCTCACGGAAACA	731	DЬ
745		686	Qy
730	AAAAGACCATTCAGTACTTGATTGGTTCTGGAATGGATCCTAGAACAGAGAACAATCCTT	671	Db
685		626	Qy
670	ACGGTGATCTTCTCAATAAGTATCTTTTACTTTGTCTGGACGTGTTGACATGAGGCAGATTG	611	Db
625		566	Qу
610	GGGCTAGCCCCACTTCATGGGCTATTTGGACAAGAGCTTGGACTGCAGAAGAGAAACCGAC	551	Db
565	GGGCTGAGCCCAGTGCTTGGGCAATGTGGACTAGGGCATGGACTGCCGAAGAAGAATAGAC	506	Qy
550	AGGCGCTTCCGACCTATCAAACCATGTTGAACACTTTGGATGGA	491	Db
505	AAGCACTTCCAACATATATGTCTATGCTCAATAGGTGTGATGGTATTAAGGATGAGACTG	446	Qy
490	GGCAAGAGAGCTCCCTGATGATTACTTCGTTGTTCTGGTGGGAGACATGATCACGGAAG	431	Db
445	GGCCAAGGAGATTCCCGACGACTATTTTGTGGTGTTAGTTGGAGATATGATCACAGAAG	386	Qy
430	ACTICITACCCGACCCTGCATCCGATGGGTTCGAAGATCAGGTTAGAGAGCTAAGAGAGAG	371	Db
385	GCAAGTGCGGGAGTTGAGG	326	Оу
370		سا	Db
325	GGGCTAGGAACAATGTGTTGATTCACCTCAAATCTGTCGAGAAATCTTGGCAACCACAAG		Qy
310		251	Db

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206 TTCAAGTCACTCACTCTATGCCACCCCAAAAGCTAGAAATATTCAAGTCCCTTGATGATT 265

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Sequence 5, Application US/08926522
; Sequence 5, Application US/08926522
; Patent No. 6426447
; GENERAL INFORMATION:
   APPLICANT: Uic C. Knauf
   APPLICANT: Gregory A. Thompson
   TITLE OF INVENTION: PLANT SEED OILS
   NUMBER OF SEQUENCES: 23
   CORRESPONDENCE ADDRESS:
   ADDRESSEE: Calgene, Inc.
   STREET: 1920 Fifth Street
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; TOPOLOGY: linear
; MOLECULE TYPE: cDN
US-08-926-522-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 38.1
Best Local Similarity 69.3
Matches 715; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: CGI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ. ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1495 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/458,173
FILING DATE: 2-June-1995
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.1
SOFTWARE: Microsoft Word 5.1(a)
CURRENT APPLICATION DATA:
                                                                                                                                                                          386
                                                                                                                                                                                                             371
431
                                                                                                                                                                                                                                                                                      311
                                                                                                                                                                                                                                                                                                                                                                              206 TTCAAGTCACTCTATGCCACCCCAAAAGCTAGAAATATTCAAGTCCCTTGATGATT 265
                                                                                                446
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                                                                                                                                                                                                                                                                                                                                                              251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
NAME: Carl J. Schwedler
REGISTRATION NUMBER: 36,924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/926,522 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: Davis
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                        GGCCTAGGAACGATGTGTTGATTCACCTCAAATCTGTCGAGAAATCTTGGCAACCACAAG 325
                                                                                                                                 GGGCCAAGGAGATTCCCGACGAACTATTTTGTGGTGTTAGTTGGAGATATGATCACAGAAG 445
                                                                                                                                                                                                                              ACTACTTGCCGGATCCGGTGTCAGACGGATTCGAGGAGCAAGTGCGGGAGTTGAGGGAAA 385
                                                        AAGCACTTCCAACATATATGTCTATGCTCAATAGGTGTGATGGTATTAAGGATGAGACTG 505
                                                                                                                                                                                                         ACTTCTTACCCGACCCTGCATCCGATGGGTTCGAAGATCAGGTTAGAGAGCTAAGAGAGA 430
                                                                                                                                                                                                                                                                                   GGGCCGAGCAGAACCTTCTAACTCAGCTCAAAGACGTGGAGAAGTCGTGGCAGCCCCAGG 370
                                                                                                                                                                                                                                                                                                                                                          TTCAAGTCCTGCATTCCATGCCACCCCAGAAGATCGAGATCTTCAAATCCATGGAAGACT 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
DEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                  38.1%; Score 511.8; DB 4; 69.3%; Pred. No. 8.8e-137; htive 0; Mismatches 308;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGNE DES
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	TCTAAAAAGGAA 1273	1262	b
		122b	QΥ
1261	AGAAAGGACCCAAGGTTCCTTTCAGCTGGATACATGACAGAGAAGTGCAGC	1211	Ъ
1225	AGAAGAAGAAGCTGAGCACCCTGTTTCTTTCAGCTGGATTTTCAATCGGGAGTTGAAGA	1166	Qy
1210	ACTTGTGTGGGTTGACTCCAAGAATCAGGAGGTTGGATGAGAAGCTCAAGCAAG	1151	DЬ
۱ 1165	ATGTGTGAATTGGGTCCCAAGATTAGGCGAAGTGGAAGAGAGAAAGTGCAAGGGAAGGAGA	1106	Qy
1150	GGAGGTGGAAGATTGAGAGCTTGACCGGGCTTTCAGGTGAAAGAAA	1091	рь
r 1105	ATAAATGGAATGTGGAAAGGCTTACGGGGCTGTCGGACGAGGGGCCGAAAAGCCGCAGGAAT	1046	Qy
1090	CTCAGAGGCTCGGTGTTTACACTGCCAAAGACTATGCGGACATTCTTGAGTTTTTGGTTG	1031	ДЬ
3 1045	CTCAGAGAGTGNGGGTTTATTCTGCGTTGGATTATTGCGACATCTTAGAGTTTCTGGTGG	986	Qy
1030	CTGCTCACTTGATGTACGATGGGCGGGATGAAAGCCTCTTTGACAACTTCTCTTTTTTTT	971	Db
3 985	CAGCGCACTTGATGTACGACGGAAGTGACGACTTCTTTTTAAACATTTCACGGGGGGTTG	926	Qy
970	TTGATCCTGATGGTACTGTGATGGCGTTTGCAGACATGATGAGGGAAGAAATCTCGATGC	911	рь
925	TCGACCCCGACACAGTAATTGCTTTTGCAGATATGATGCGCAAAAAAATAACAATGC	866	Qy
1 910	CTGCAGACGAGAAGCGTCATGAGACAGCTTACACCAAGATAGTTGAGAAGCTCTTTGAGA	851	ФФ
1 865	CCTCCGACGAGAAGCGCCACGCCACAGCCTACACCAAGATCGTGGAAAAAGCTCGCTGAGA	806	Qy
850	CAGCTCGCCAAGCCAAAGCACGGAGACCTCAAGCTAGCCCAAATCTGCGGCACAATAG	791	Дb
805	CAGCCAAGCTGGCCCAACACTACGGCGACAAGAACCTCGCTCACATCTGCGGCTCCATCG	746	Qy
790	ACCTCGGCTTCATCTACACTTCATTCCAAGAAAGAGCCACCTTCATCTCTCACGGAAACA	731	Db
745	ACCTAGGCTTCATCTACACATCCTTCCAAGAGAGAGAGCAACCTTCATATCCCCATGCCAACA	686	Оу
730	AAAAGACCATTCAGTACTTGATTGGTTCTGGAATGGATCCTAGAACAGAGAACAATCCTT	671	DЬ
1 685	AGAAGACTATTCAATATCTCATCGGCTCAGGAATGGATATCAAGTCAGAAAAACAGCCCCT	626	Qy
670	ACGGTGATCTTCTCAATAAGTATCTTTACTTGTCTGGACGTGTTGACATGAGGCAGATTG	611	DЬ
625	ATGGTGACCTTCTCAATAAGTACCTTTATTTGTCTGGAAGGGTTGATATGAGGAAAATTG	566	ΟУ
; 610	GCGCTAGCCCCACTTCATGGGCTATTTGGACAAGAGCTTGGACTGCAGAAGAGAGAACCGAC 610	551	Вþ

Search completed: December 2, 2002, 00:41:48
Job time: 84 secs

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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                      Result
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Maximum DB seq length: 200000000
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ALIGNMENTS

RESULT 1 AAQ92889 ID AAQ9

AAQ92889 standard; cDNA; 1309 BP

Coriander omega-12 desaturase cDNA

05-DEC-1995 AAQ92889;

(first entry)

Coriander; omega-12 desaturase; petroselenic acid; transgenic plant; crop improvement; tobacco; ss.

a

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CDS
                                                              sig_peptide
07-AUG-1992;
         07-AUG-1992;
                  04-JUL-1995
                                                mat_peptide
                                                                                        Coriandrum sativum
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Matches 762
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ATGATGAGGAAGAAATACAAATGCCAGCTCATGCAATGTACGATGGCTCCGATGATATG
                              ATGATGCGCAAAAAATAACAATGCCAGCGCACTTGATGTACGACGGAAGTGACGAACTT
                                                                                    AAGATCGTGGAAAAGCTCGCTGAGATCGACCCCGACACAACAGTAATTGCTTTTGCAGAT
                                                                                                                                    CTAGCTCAAGTGTGTGGCAACATTGCTTCTGACGAGAAACGCCATGCCACCGCCTACACC
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                                                                  AAAATCGTGGAGAAGCTTGCGGAGATTGACCCAGACACCACTGTTATCGCATTTTCTGAC
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Query Match

Sequence

1643 for

BP;

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383 invention

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0 other; 20;

42

78;

Score

573 G; 477

Length

the

methods of the

The specification describes methods for introducing localized mutations into target genes in plant cells. The methods comprise using a recombinogenic oligonucleobase comprising 2 regions homologous to a target gene and an intervening mutant region. The methods can be used to introduce localized mutations into target genes to introduce desirable traits, e.g. selective growth advantage under appropriate selective conditions, change in colour of plant cells growing in a callus, bestelding a colour of plant cells growing in a callus.

herbicide resistance, or improved preservation of fruit or flowers. They can be used in plants such as maize, wheat, rice, lettuce, potato, tomato, canola, soybean or cotton cell. The present sequenc represents

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                                                   GACGAACTTCTTTTTAAACATTTCACGGCGGTTGCTCAGAGAGTGNGGGTTTATTCTGCG
                                                                                   TTTGCTGATATGATGAGAAAAATTTCTATGCCTGCACACTTGATGTATGATGGCCGA
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16-MAR-1990;
13-AUG-1990;
14-NOV-1990;
14-MAR-1991;
The present sequence encodes a Ricinus communis desaturase from clone pCGN3230. The present invention describes a recombinant DNA construct comprising a DNA sequence encoding a plant Delta-9 desaturase protein. The present invention also provides a method of modifying fatty acid composition in a host plant cell from a given fatty acid saturation to a different fatty acid saturation, comprising growing a host plant cell containing a recombinant DNA sequence which encodes a plant cell containing a recombinant DNA sequence which encodes a plant
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                                                                                                                                                                                                                                                                            DNA encoding plant delta-9 desaturase protein - having amino acid sequence of Carthamus tinctorius desaturase, useful for, e.g. producing oil-seeds with modified levels of fatty acid saturation
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90US-0494106.

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TCTTGGAGTCTACACAGCAAAGGATTATGCAGATATATTGGAGTTCTTGGTGGGCAGATG
            AGTGNGGGTTTATTCTGCGTTGGATTATTGCGACATCTTAGAGTTTCTGGTGGATAAATG
                                                                     CTTGATGTACGACGGAAGTGACGAACTTCTTTTAAACATTTCACGGCGGTTGCTCAGAG
                                                                                                                                                                                          ACAAGCCAAAGAGCATGGAGACATAAAGTTGGCTCAAATATGTGGTACAATTGCTGCAGA
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                                                                                                                                                                                                            14-NOV-1990;
16-MAR-1990;
13-AUG-1990;
                        A desaturase was purified from C. tinctorius and sequenced. Based on this sequence, oligonucleotide probes were synthesised and used to screen a C. tintorius embryo cDNA library to obtain DNA (AAQ13963) encoding the desaturase. The DNA for the C. tinctorius desaturase was also used as a probe to isolate DNA encoding desaturase from Ricinus communis (AAQ13964), Brassica campestris (AAQ13965) and Simmondsia chinensis (AAQ13966).
Sequence
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                                                                                                   Disclosure;
                                                                                                                 DNA encoding a plant desaturase - used for modify fatty acid compsn. of plant cells and plant seeds
                                                                                                                                                         WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ13964;
                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ13964 standard; DNA;
                                                                                                                                               P-PSDB; AAR14189
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Query Match Best Local S Matches 821

Local Similarity mes 821; Conserv

Conservative

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Mismatches

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Score 568.8; DB 12 Pred. No. 8.4e-150;

DB 12;

Length 1668;

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GAAAGCTGAGCACCCTGTTTCTTTCAGCTGGATTTTCAATCGGGAGTTGAAGATATGAAC
                                                  TGAATTGGGTCCCAAGATTAGGCGAGTGGAAGAGAAAGTGCAGGGGAAGGAGAAGAAGAA :L172
                                                                                                                                        AGTGNGGGTTTATTCTGCGTTGGATTATTGCGACATCTTAGAGTTTTCTGGTGGATAAATG
                                                                                                                                                                                                                                                                   CTTGATGTACGACGGAAGTGACGAACTTCTTTTTAAACATTTCACGGCGGTTGCTCAGAG
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                                 GAAGGTGGATAAACTAACGGGCCTTTCAGCTGAGGGACAAAAGGCTCAGGACTATGTTTG
                                                                                                                                                                          TCTTGGAGTCTACACAGCAAAGGATTATGCAGATATATTGGAGTTCTTGGTGGGCAGATG
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201 AAATCTTCAAGTCACTCACTCTATGCCACCCCAAAAGCTAGAAATATTCAAGTCCCTTGA 260

Query Match Best Local Sim Matches 741;

Similarity

41.48; 72.18;

Score 555.8;

Conservative

0

Mismatches

Length Indels

9;

Gaps

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1092;

Pred.

No.

5.8; DB 22; 3.1e-146; ches 278;

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RESULT 5
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                                                                                                                                                                    New mutant castor Delta9-18:0-Acyl Carrier Protein desaturase, useful in producing commercially valuable products, e.g. vegetable oils useful
                                                                                                                                                                                                                    Shanklin
                                                                                                                                                                                                                                                                                                                                                    Ricinus
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Sequence 1092 BP; 318 A; 214 C;
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                                       AATGCCAGCGCACTTGATGTACGACGGAGGTGACGAACTTCTTTTTAAACATTTCACGGC
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                                                                                           GGAATATGTGTGTGAATTGGGTCCCAAGATTAGGCGAGTGGAAGAGAAAAGTGCAGGGGAA
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                                                                                                                                                                            GGTTGCTCAGAGAGTGNGGGTTTATTCTGCGTTGGATTATTGCGACATCTTAGAGTTTTCT
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GAAGCTGT
                                                                                GGTGGGCAGATGGAAGGTGGATAAACTAACGGGCCTTTCAGCTGAGGGACAAAAGGCTCA
                                                                                                                                                                  TGTTGCGCAGCGTCTTGGAGTCTACACAGCAAAGGATTATGCAGATATATTGGAGTTCTT
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                                                                                                                                                                                                                           The cDNA comprises a poly(A) track at the 3' end of 100-200 bases. A desaturase was purified from C. tinctorius and sequenced. Based on this sequence, oligonucleotide probes were synthesised and used screen a C. tintorius embryo cDNA library to obtain DNA encoding t desaturase. The DNA for the C. tinctorius desaturase was also use a probe to isolate DNA encoding desaturase from Ricinus communis (AAQ13964), Brassica campestris (AAQ13965) and Simmondsia chinensi
                                                                                                                                                                                                                                                                                                                                                                                                                                             14-NOV-1990;
16-MAR-1990;
13-AUG-1990;
                                                                                                                                                                                                                                                                                                                                    DNA encoding a plant desaturase - fatty acid compsn. of plant cells
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hes 739; Conser
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                                ATTCACCTCAAATCTGTCGAGAAATCTTGGCAACCACAAGACTACTTGCCGGATCCGGTG
                                                                        CCACCCCAAAAGCTAGAAATATTCAAGTCCCTTGATGATTGGGCTAGGAACAATGTGTTG
 TCAGACGGATTCGAGGAGCAAGTGCGGGAGTTGAGGGAAAAGGGCCAAGGAGATTCCCGAC
                     GTTCACCTAAAGCCAGTGGAGAAATGTTGGCAAGCACAGGATTTCTTGCCGGACCCTGCA
                                                                                                      AATGCCAAGAAGCCTTTTCAACCTCCACGAGAGGTTCATGTTCAGGTGACGCACTCCATG
                                                              CCACCAGAAGATAGAGATTTTCAAATCCATCGAGGGTTGGGCTGAGCAGAACATATTG
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                                                                                                                                                Conservative
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Pred. No. 1.3e-136,
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                    synthesis; seed; acyl carrier protein;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            The desaturase gene isolated from Carthamus tinctorius was present as the clone pCGN2754. The clone can be used to construct, acyl carrier protein expression cassettes in a binary vector for plant transformation. This allows integration of nucleic acids encoding a desaturase sequence and a synthase sequence into the genome of a host cell. A plant desaturase includes any enzyme capable of catalysing the insertion of a first double bond into a fatty acid calcaly specially between C9 and C10.
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1533 BP; 421 A; 327 C; 391 G; 394 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Fig
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15-AUG-1990;
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TACCTTTATTTGTCTGGAAGGGTTGATATGAGGAAAATTGAGAAGACTATTCAATATCTC
                                       GCAATGTGGACTAGGGCATGGACTGCCGAAGAGAATAGACATGGTGACCTTCTCAATAAG
                                                                          ACAATGCTTAATACCCTAGATGGTGTACGTGATGAGACTGGGGGCTAGCCCTTACGCCTTGG
                                                                                         TCTATGCTCAATAGGTGTGATGGATTAAGGATGAGACTGGGGCCTGAGCCCAGTGCTTGG
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                          GCTGTCTGGACTAGGGCTTGGACAGCTGAAGAGAACAGGCATGGCGATCTTCTCCACACC
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Pred. No. 1.3e-136;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Higher plants appear to share a common metabolic pathway for the synthesis of fatty acids. Genes encoding synthase proteins may be used in nucleic acid constructs to modulate the amount of synthase activity in a host cell. Nucleic acid constructs may also be designed to decrease the expression of a synthase protein, i.e., constructs containing anti-sense synthase sequences. The construct allow the generation of plants bearing seeds which have enhanced oillow the generation of plants bearing seeds which have enhanced of common plant unsaturated fatty acids is catalysed by a desaturase. It incleic and alpha-linoleic acids found in storage triglycerides are produced from the desaturation of stearoyl-ACP to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1533 BP; 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA constructs encoding beta-keto:acyl-ACP modify the oil content of seeds, e.g. for c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Sines 739;
             TACCTTTATTTGTCTGGAAGGGTTGATATGAGGAAAATTGAGAAGACTATTGAATATCTC
                                                                                                                                                                             GCAATGTGGACTAGGGCATGGACTGCCGAAGAGAATAGACATGGTGACCTTCTCAATAAG
                                                   ATTGGGTCAGGAATGGATCCTCGTACCGAAAACAGCCCCTACCTTGGGTTCATCTACACA
                                                                 ATCGGCTCAGGAATGGATATCAAGTCAGAAAACAGCCCCTAGCCTAGGCTTCATCTACACA
                                                                                                          TATCTCTACCTTTCTGGGCGGGTAGACATGAGGCAGATACAGAAGACAATTCAGTATCTC
                                                                                                                                                               CTGTCTGGACTAGGGCTTGGACAGCTGAAGAGAACAGGCATGGCGATCTTCTCCACACC
                                                                                                                                                                                                                      ACAATGCTTAATACCCTAGATGGTGTACGTGATGAGACTGGGGCTAGCCTTACGCCTTGG
                                                                                                                                                                                                                                      TCTATGCTCAATAGGTGTGATGGTATTAAGGATGAGACTGGGGCTGAGCCCAGTGCTTGG
                                                                                                                                                                                                                                                                           GACTATTTTGTGGTGTTAGTTGGAGATATGATCACAGAAGAAGCACTTCCAACATATATG
                                                                                                                                                                                                                                                                                                                                                  TCAGACGGATTCGAGGAGCAAGTGCGGGAGTTGAGGGAAAGGGCCAAGGAGATTCCCGAC
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1.3e-136;
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                                                             16-SEP-1991;
16-MAR-1990;
13-AUG-1990;
14-NOV-1990;
14-MAR-1991;
06-JUN-1995;
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GCCACAGCCTACACCAAGATCGTGGAAAAGCTCGCTGAGATCGACCCCGACACACAGTA
                             CATGGGGACGTGAAACTGGCGCAAATTTGTGGTACAATCGCGTCTGACGAAAAGCGTCAC
                                             TACGGCGACAAGAACCTCGCTCACATCTGCGGCTCCATCGCCTCCGACGACGAAGAAGCGCCAC
                                                                                       TCGTTTCAAGAGCGTGCCACATTTGTTTCTCACGGAAACACCGCCAGGCATGCAAAGGAT
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                 The specification describes methods for introducing localized mutations into target genes in plant cells. The methods comprise using a recombinogenic oligonucleobase comprising 2 regions homologous to a target gene and an intervening mutant region. The methods can be used to introduce localized mutations into target genes to introduce desirable traits, e.g. selective growth advantage under appropriate selective conditions, change in colour of plant cells growing in a callus, herbicide resistance, or improved preservation of fruit or flowers.
                                                                                                                                                                                                                                                                                                                     Introducing mutations into target genes in plant cells recombinggenic oligonucleobase comprising 2 regions how
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             TACGGCGACAAGAACCTCGCTCACATCTGCGGCTCCATCGCCTCCGACGAGAAGCGCCCAC
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                                                             TCTGCGTTGGATTATTGCGACATCTTAGAGTTTCTGGTGGATAAATGGAATGTGGAAAGG
                                                                                            GGGCGTGATGACAACCTCTTCGAACATTTCTCGGCGGTTGCCCCAAAGACTCGGCGTCTAC
                                                                                                                   GGAAGTGACGAACTTCTTTTAAACATTTCACGGCGGTTGCTCAGAGAGTGNGGGTTTAT
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                                                                                                                                                                                                                                                                                                                                                                                   TATCTCTACCTTTCTGGGCGGGTAGACATGAGGCAGATACAGAAGACAATTCAGTATCTC
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RESULT 11
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transform Umbelliforae plants, pref. Brassica napus and rapus plants. The antisense delta-9-desaturase construct acts to downregulate the delta-9-desaturase without downregulating the PAPD. The transformed plants may be cultured to produce petroselinic acid which is an isomer of oleic acid. Unlike oleic acid, petroselininc acid may be refined by ozonolysis to give lauric acid and adipic acid which are useful for polymerisation to nylon and other high value polymers. The petroselining acid may therefore be used as an industrial feedstock in the manufacture
                                                                                                                                                                                                                                                  This sequence represents the B. napus delta-9-desaturase gene. This sequence was used to transform a plant such that an antisense constraint such that an antisense constraint such that an antisense constraint such that the production with the petroselinic acid producing used in conjuction with the petroselinic acid producing desaturase (PAPD) enzyme gene from coriander. The PAPD envisor originally thought to be a delta-9-desaturase, however the invertibility in the particular of the producing on a palmityl-acyl carrier protein, and would therefore be a palmitate desaturase rather than a stearoyl desaturase. The PAPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               delta-9-desaturase; delta-4-desaturase; palmityl-acyl carrier protein; palmitate desaturase; stearoyl desaturase; antisense; Umbelliforae; Brassica napus; Brassica rapus; downregulate; isomer; oleic acid; refine; ozonolysis; lauric acid; adipic acid; polymerisation; nylon;
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                                                                                                                                                                                                sequence and the antisense delta-9-desaturase construct may be used to transform Umbelliforae plants, pref. Brassica napus and rapus plants.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA encoding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Delta-9-desaturase
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                                          AATATGTGTGTGAATTGGGTCCCAAGATTAGGCGAAGGAGAAGAGAAAGTGCAGGGGAAGG
                                                                                            TGGATAANTGGAATGTGGAAAGGCTTACGGGGCTGTCGGACGAGGGGCGAAAAGCGCAGG
                                                                                                                                               TTGCTCAGAGAGTGNGGGTTTATTCTGCGTTGGATTATTGCGACATCTTAGAGTTTCTGG
                                                                                                                                                                                                                                                                                                      TCGCCTCCGACGAGAAGCGCCACGCCACAGCCTACACCAAGATCGTGGAAAAGCTCGCTG
                                                                                                                                                                                                                                                                                                                                                                                                            CCTACCTAGGCTTCATCTACACATCCTTCCAAGAGAGCAACCTTCATATCCCATGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACATGGTGACCTTCTCAATAAGTACCTTTATTTGTCTGGAAGGGTTGATATGAGGAAAA
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  AGAAGAA 1169
                                                                             CCGGGAGGTGGAGGATCGAGAGCTTGACTGGGCTTTCGGGTGAAGGGGAACAAAGCGCAAG
                                                                                                                                                                                                 TGCCAGCGCACTTGATGTACGACGAAGTGACGAACTTCTTTTAAACATTTCACGGCGG
                                                                                                                                                                                                                                                                                                                                                          ACACAGCCAAGCTGGCCCAACACTACGGCGAAGAACATCTGCTCACATCTGCGGCTCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTGAGAAGACTATTCAATATCTCATCGGCTCAGGAATGGATATCAAGTCAGAAAACAGCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCACGGTGATCTTCTCAATAAGTATCTTTACTTGTCTGGTCGTTGACATGAGGCAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CTGGGGCTGAGCCCAGTGCTTGGGCAATGTGGACTAGGGCATGGACTGCCGAAGAGAATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAAGGGCCAAGGAGATTCCCGACGACTATTTTGTGGTGTTAGTTGGAGATATGATCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTGGGCTAGGAACAATGTGTTGATTCACCTCAAATCTGTCGAGAAAATCTTGGCAACCAC
                           TGGCTCAGAGGCTCGGTGTTTACACTGCCAAAGACTATGCGGACATTCTTGAGTTTTTGG
                                                                                                                                                                                   TGCCTGCTCACTTGATGTACGATGGGCGTGATGATAACCTCTTTGACAACTTCTCCTCCG
                                                                                                                                                                                                                                      AGATTGATCCTGACGGCACTGTGGTGGCCCTTTGCGGATATGATGAGGAAGAAAATCTCGA
                                                                                                                                                                                                                                                              TAGCTGCAGACGAGAAGCGTCACGAGACAGCTTACACCAAGATAGTTGAGAAGCTTCTCG
                                                                                                                                                                                                                                                                                                                                           ACACAGCTCGCCAAAGCCAAAGAGCACGGAGACCTCAAGCTAGCGCAAATCTGCGGGACAA
                                                                                                                                                                                                                                                                                                                                                                                              CTTACCTTGGCTTCATCTACACTTCATTCCAAGAGAGCCACCTTCGTCTCTCACGGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                  TTGAAAAGACTATTCAGTACCTGATTGGTTCCGGAATGGATCCAGCGACAGAACAACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CTGGCGCTAGCCCCACTTCATGGGCCGTTTGGACTAGAGCTTGGACCGCTGAAGAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              405
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71.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 521.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              407 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .6e-1
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279;
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В

1168

CCAAGAA

1174

Q DЬ

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RESULT 12
AAT63437
Дb
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                                                                        Qy
                                                                                                      Db
                                                                                                                              δÃ
                                                                                                                                                                                                          Matches
                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                                                 A cDNA clone (AAT63437), designated BND11, codes for oilseed rape stearoyl-ACP desaturase (AAW14797), an enzyme that catalyses the desaturation of stearoyl-ACP (C18:0) to oleoyl-ACP (C18:1). BND11 and clone BND9 (see also AAT63438) were isolated from a cDNA library constructed from RNA obtd. from mid maturation seeds of Brassica napus cv. 212/86. The library was screened with the coding region of a delta-9 desaturase gene from Brassica campestris. An antisense gene was constructed to generate antisense RNA homologous to both BND9 and BND11. In transgenic Brassica plants expressing the
                                                                                                                                                                                                                                                                                                                                                                                                                             Increasing levels of stearate in plant seed triglyceride(s) using a DNA sequence encoding acyl-ACP thioesterase protein substantial activity on C18:0 acyl-ACP substrates
                                                                                                                                                                                                                                stearoyl-ACP desaturase antisense construct and mangosteen Class I acyl-ACP thioesterase GarmFatAl (see also AAW14795), levels of Cl8:0 in the seed oil may exceed 50% of total fatty acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                        Example 5; Fig6A-6C; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             03-APR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         antisense;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stearoyl-ACP desaturase; rapeseed; acyl-ACP thioesterase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAT63437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1997-212906/19.
P-PSDB; AAW14797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Knauf VC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (CALJ ) CALGENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-SEP-1996;
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335
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                                                                                                                  TTCAAGTCACTCATGTGCCACCCCAAAAGCTAGAAATATTCAAGTCCCTTGATGATT
            ACTACTTGCCGGATCCGGTGTCAGACGGATTCGAGGAGCAAGTGCGGGAGTTGAGGGAAA
                                                                GGGCTAGGAACAATGTGTTGATTCACCTCAAATCTGTCGAGAAATCTTGGCAACCACAAG
                                                                                                    TTCAAGTCCTGCACTCCATGCCACCCCAAAAGATCGAAATCTTCAAATCCATGGAAGACT
                                                                                                                                                       bal Similarity
687; Conserv
ACTTCTTACCGGACCCTGCTTCCGACGGGTTCGAAGACCAGGTAAAAGAGTTAAGAGAAA
                                                 GGGCCGAGCACCACCTCCTACCTCAACCTCAAAGACGTGGAGAAGTCATGGCAGCCCCAGG
                                                                                                                                                                                                          1529
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oil;
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                                                                                                                                                         Conservative
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                                                                                                                                                                                                          BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25..1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                        414 A; 351 C; 363 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA;
                                                                                                                                                                   38.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lassner
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       stearic acid;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Garcinia
                                                                                                                                                       Score 521.4;
Pred. No. 1.9e
0; Mismatches
                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ВP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mangifera;
                                                                                                                                                                                                        401 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic plant; oilseed;
                                                                                                                                                       1; DB 18;
1.9e-136;
nes 277;
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                                                                                                                                                                              Length
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                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                          having
                                                                                                                                                      Gaps
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                                                 334
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DЬ Qy 밁 δÃ В Qy Вb ρy Db Qy В Qy DЬ δÃ В Qy DЬ Qy В Qy Вb Qγ Ъ QΥ Вþ QΥ

Glycine max strain Cultivar

Location/Qualifiers

soya bean; plant oil;

stearic acid;

SS coding

desaturase

sequence

from

pDS1

31-MAR-1992

(first entry) stearoyl-ACP

AAQ20187

AAQ20187 standard;

CDNA

to

mRNA;

2243

ВР

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RESULT 13
AAQ20187
ID AAQ20
XX
AC AAQ20
XX
AC AAQ20
XX
BT 31-MA
XX
DE Soybe
XX
XX
Soybe
XX
Soya
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Soya
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FH Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CC A Lambda ZAP cDNA library was prepared from soybean embryos polyA RNA CC and used to infect E.coli BB4 cells. The cells were plated and control transferred to nitrocellulose filters for hybridisation. Probes were called based on the N-terminal amino acid sequence of purified control plaque purification and the regions of each vector comprising the coll transfer were excised. The resulting phagemids were used to infect E.coli XL-1 Blue cells to give 6 double-stranded plasmids composed to the coll transfer were excised. The invention covers chimeric compositing uncleotides 1-2243, 70-1245 or 16-1245 of this sequence, linked to suitable control sequences. They are used for transforming oil-producing plant cells to produce antisense in the seed, overexpress precursor desaturase in the seed overexpress precursor desaturase in the seed overexpress precursor desaturase in the calls to produce antisense in the seed overexpress precursor desaturase in the seed overexpress precursor desaturase in the seed overexpress precursor desaturase in the calls to produce antisense in the seed over plants of the produce antisense in the seed over plants of the plant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2243 BP;
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CCAGTGACCAGAGTTAGCTCTCCAAGGGTTTTCATGGCTTCCACTGTCAACTCTAACTCC 171
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                                      CCGGATCCGGTGTCAGACGGATTCGAGGAGCAAGTGCGGGAGTTGAGGGAAAAGGGCCAAG
                                                                            CAGAACATCTTGACTCATCTTAAACCTGTAGAAAAATGTTGGCAACCACAGGATTTTTTA
                                                                                                 AACAATGTGTTGATTCACCTCAAATCTGTCGAGAAATCTTGGCAACCAAGACTACTTG
                                                                                                                                                           ACTCACTCTATGCCACCCCAAAAGCTAGAAATATTCAAGTCCCTTGATGATTGGGCTAGG
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                             Soybean stearoyl ACP-desaturase gene; chimeric gene; ant transformation; saturated fatty acid; unsaturated fatty
                                                                Nucleotide
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                                                              of the soybean seed stearoyl-ACP desaturase
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19-MAY-1991;
11-DEC-1992;
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                                                                                                                                                                                                                                                                          This is the nucleotide sequence of the soybean stearoyl ACP-desaturase gene, used in the method of the invention, which involves the creation of chimeric genes which are used in (antisense orientation) to transform plant cells. The nucleic acids are useful for controlling the levels of (un)saturated fatty acids in soybean oil. In transformed cells (seeds), the chimeric genes transcribe the antisense RNA to the complementary mRNA for the enzyme. This results in inhibition of expression of the endogenous enzyme and reduction in desaturates and polyunsaturates and high in monosaturates, giving an oil
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CCGGATCCGGTGTCAGACGGATTCGAGGAGCCAAGTGCGGGAGTTGAGGGAAAGGGCCAAG
                                CAGAACATCTTGACTCATATTTTAAACCTGTAGAAAAATGTTGGCAACCACGGATTTTTTA
                                          AACAATGTGTTGATTCACCTCAAATCTGTCGAGAAATCTTTGGCAACCACAAGACTACTTG
                                                                         ACTCACTCTATGCCACCCCAAAAGCTAGAAATATTCAAGTCCCTTGATGATTGGGCTAGG
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RESULT 15
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Cotton; delta9-desaturase; fatty acid delta12-desaturase; linoleic acid; stearic acid; oleic acid; transgenic plant cotton seed oil; stearoyl-ACP delta9-desaturase; SAD-1; s:

plant;

palmitic

acid

Cotton

stearoyl-ACP

delta9-desaturase (ghSAD-1)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Modifying endogenous oil of cotton plants, to produce cotton with reduced palmitic and/or linoleic acid content, involves transgenic plants containing a fatty acid biosynthesis gene i construct.
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SUMMARIES

SOURCE ORGANISM REFERENCE AUTHORS TITLE	RESULT 1 A74271 LOCUS DEFINITION ACCESSION VERSION KEYWORDS		1 613. 2 613. 3 513. 4 573. 5 57. 7 564. 11 5 26. 11 5 26. 12 5 27. 13 5 27. 14 5 27. 15 5 27. 16 5 27. 17 5 28. 18 5 29. 19 5 27. 20 513. 22 513. 23 513. 24 513. 25 512. 26 512. 27 511. 28 511. 29 511. 30 511. 31 508. 32 508. 33 508. 34 499. 44 493. 45 499. 46 493. 47 493. 48 493. 48 93.	Result No. Sc
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Cahoon, E.B. and Ohlrogge, J.B.
Metabolic evidence for the involvement of a delta-4-palmitoy carrier protein desaturase in petroselinic acid synthesis in coriander endosperm and transgenic tobacco cells
Plant Physiol. 104, 827-837 (1994)
                                                                                                                                            Expression of a coriander desaturase production in transgenic tobacco Proc. Natl. Acad. Sci. U.S.A. 89 (23)
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ATFISHANTAKLAQHYGDKNLAQVCGNIASDEKRHATAYTKIVEKLAEIDPDTTVIAF
SDMMRKKIQMPAHAMYDGSDDMLFKHFTAVAQQIGVYSAWDYCDIIDFLYDKWNVAKM
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/db_xref="taxon:4047"
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Shanklin,J. and Somerville,C.
Stearoyl-acyl-carrier-protein desaturase from higher plants structurally unrelated to the animal and fungal homologs proc. Natl. Acad. Sci. U.S.A. 88 (6), 2510-2514 (1991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M59857.1 GI:169716 fatty acid synthetase; lipid metabolism; stear protein desaturase. Ricinus communis developing seed cDNA to mRNA.
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                                                                 HLKPVEKCWQPQDFLPDPASDGFDEQVRELRÊRAKEIPDDYFVVLVGDMITEEALPTY
QYMLNILDGVRDETGASFTSWALWTAWYAEENHEIDLLKYLYLVLSGRVDMRQIEKTI
QYLLGSCMDPRTENSFYLGETYTSCDERATEISHGNTAKQAKEHGDIKLAQIGGTIAA
QYLLGSGMDPRTENSFYLGETYTSCDERATEISHGNTAKQAKEHGDIKLAQIGGTIAA
DEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDHFSAV
AQRLGVTTAKDYADILEFLVGRWKVDKLTGLSAEGQKAQDYVCRLPPRIRKLEERAQG
RAKKAPTMPESMIFDRQVKLT

321 c 383 g 477 t
                                                                                                                                                             /product="stearoyl-acyl-carrier protein desaturase"
/protein_id="AAA74692.1"
/protein_id="AAA74692.1"
/db_xref="GI:951427"
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PKFYMASTLKSGSKEVENLKKPPMPPREYHVQVTHSMPPQKIEIFKSLDNWAEENILV
                                                                                                                                                                                                                                               /dev_stage="developing" <1. .1239
                                                                                                                                                                                                                                                                       /organism="Ricinus co
/db_xref="taxon:3988"
/tissue_type="seed"
                                                                                                                                                                                                                                   /codon_start=1
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Score 573.8;
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0; Mismatches
e 573.8; DB 8;
. No. 6.6e-129;
ismatches 393;
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Direct Submission

Submitted (08-NOV-1990) D.S. Knutzon, CALGENE INC, 1920 FIF-

STREET, DAVIS CA 95616, USA

2 (bases 1 to 1662)

Knutzon,D.S., Scherer,D.E. and Schreckengost,W.E.

Nucleotide sequence of a complementary DNA clone encoding

Nucleotide sequence of a complementary DNA clone encoding
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Ricinus communis
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
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1 (bases 1 to 1668)

Thompson,G.A. and Knauf,V.C.
Plant desaturases -- compositions and Patent: US 5723595-A 15 03-MAR-1998;
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                           Direct Submission
Submitted (12-NOV-1994) Kyoji Yamada, Toyama University, Facu
Science, Biology; Gofuku 3190, Toyama, Tayama 930, Japan
(B-mail:yamada@sci.toyama-u.ac.jp, Tel:0764-41-1271(ex.2335),
Fax:0764-41-2972)
                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Pedallaceae; Sesamum.

1 (bases 1 to 1580)

1 (bases 1 to 1580)

1 (vikawa, Y., Takaiwa, F., Shoji, K., Masuda, K. and Yamada, K. Structure and expression of two seed-specific cDNA clones encoding stearcyl-acyl carrier protein desaturase from sesame, Sesamum
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/clone_lib="lambda g
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/strain="4294"
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/product="stroy1 acy1 carrier protein"
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                                                                                             4 . .1194
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/db_xref="taxon:4182"
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                                           CTTGATGTACGACGGAAGTGACGAACTTCTTTTAAACATTTCACGGCGGTTGCTCAGAG
                                                                              TGAGAAGCGTCATGAAAACTGCATACACCAAGATAGTGGAAAAGCTATTTGAGATTGACCC
                                                                                                                                                                                                                                           ATTTATCTATACATCCTTCCAAGAAAGGGCTACTTTCATCTCCCATGGCAACACTGCAAG
                                                                                                                                                                                                                                                                                                 CTTCCGGTATCTGATAGGATCAGGAATGGATCCACGGACAGAAAACAGCCCATATCTTGG
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 AGTGNGGGTTTATTCTGCGTTGGATTATTGCGACATCTTAGAGTTTCTGGTGGATAAATG
                                                                                                                                                                                        ACTTGCAAGGGAACATGGGGACTTGAAGCTGGCCCAAATCTGCGGCACAATTGCCGCAGA
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YLGFILTTSFQERATFISHGNTARLAREHGDLKLAQIGGTIAADEKRHETAYTKIVEKL
FEIDPNDTYLAFADMMRKKISMPÄHLMYDGRDDNLFDHFSSVAQRLGVYTAKDYADIL
EHLVARWKVANLTGLSADGQKAQDYVCGLPPRIRRLEERAQGRAKQAPKIPFSWVHDR
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0; Mismatches
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                                                                                                                              254
                                                                                                                                                                                                        194 CAAGTCTCAGATCTCCTAAGTTTGTTATGGCCTCCACTCTCCGCTCCACCTCCAGGGAGG
TGTTGATTCACCTCAAATCTGTCGAGAAATCTTGGCAACACACAAGACTACTTGCCGGATC
                                                     TGAATTGGGTCCCAAGATTAGGCGAGTGGAAGAAGTGCAGGGGAAGGAGAGAA 1169
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                                                                                         CTATGCCACCCCAAAAGCTAGAAATATTCAAGTCCCTTGATGATTGGGCTAGGAACAATG
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                                                                                                                            TTGAGACGCTTAAGAAACCCTTTATGCCTCCAAGGGAAGTGCATCTTCAAGTAACTCACT
                                                                                                                                                                    TTGATAATCTCAAAAGTCCGCCAA-----
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Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;
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124. .222
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/product="stearoy1-acy1-carrier protein desaturase"
/product="stearoy1-acy1-carrier protein desaturase"
/protein_id="aAA33130.1"
/db_xref="GI:167536"
/translation="MALKFHFITSQSPKLPSFRNPQLASLRSPKFVMASTLRSTSREV
/translation="MALKFHFITSQSPKLPSFRNPQLASLRSPKFVMASTLRSTSREV
ETLKKPFMPPREVHLQVHSMPPPQKMEIFKSLEDWAEENLLVHLKPVERCWQPQDFLP
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SPTPWALWTRAWTAEENRHGDLLNKYLYLSGRVDMRQVEKTIQYLIGSGMDPRTENNP
YLGFIYTSFQERATFISHGNTARLAKEHGDIKLAGJGGTTAADEKRHETAYTKIVEKL
YLGFIYTSFQERATFISHGNTARLAKEHGDIKLAGJGGTTAADEKRHETAYTKIVEKL
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296 c 350 g 343 t
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EFLVGRWKVESLTGLSGEGQKAQDYVCALPARIRKLEERAQGRAKEGPTIPFSWIFDR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Cucumis sativus"
/db_xref="taxon:3659"
/tissue_type="cotyledon"
/dev_stage="seedling"
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                                                                                               GAGTAGGAAGGAAGAATGTG
                                                                                                                       GAAGGGAATGGAGGAGCAAATG 1261
                                                                                                                                                                                                                      TTTATTCTGCGTTGGATTATTGCGACATCTTAGAGTTTCTGGTGGATAAATGGAATGTGG
                                                                                                                                                                                                                                                                                                                                              ACGATGGCCGCGACGACACTTGTTCCATCACTTCTCAGCAGTTGCACAGAGGCTTGGAG
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                                                            AAATGCCCGCAACCTCAGGATTTCCTGCCCGACCCAGCTTCTGATGAATTTCATGATCAG
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A Determinant of Substrate Specificity Predicted
Desaturase of Developing Doxantha Seed
Plant Physiol. (1998) In press
2 (bases 1 to 1509)
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Macfadyena unguis-cati
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sprswalwtrawtaeenrhgdbyfvvlvgmhTedalptvflytlgsgmbfrfensp
ylgfstytspgarentfablakbltsgrvbmkgiektigVtligsgmbprtensp
ylgfstytspgraffishgntarlakbltgdrdncfdflasdekrhetatytklvkl
feidpbgtvlargdmxkkismedhfpktdgrdnkfdhessvaqrlgvvtakbyadil
ehlvgrwkvekltglsaeggkagdvvcglpprirrleeraqirakQaprlpfswiydr
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/db_xref="taxon:73871"
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  Cahoon,E.B., Becker,C.K., Shanklin,J. and Ohlrogge,J.B. cDNAs for isoforms of the delta 9-stearoyl-acyl carrier desaturase from Thunbergia alata endosperm Plant Physiol. 106 (2), 807-808 (1994)
                                             Thunbergia alata.
Thunbergia alata
Thunbergia alata
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Acanthaceae; Thunbergia.
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                                                                                                                                         ACCTTAGATGTGTGCGGGATGAAACAGGAGCGAGCCCAACTCCTTGGGCCAATTTGGACA
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/db_xrof="G1:533082"
/translation="TILREVETANKHETPPSEVHVQVTHSMPPQKIEIFKSLEDWAAD
NILVYLKPVEKCWQPQDFLPDPASDGFHDQVKELRERAREIPDDYFVVLVGDMITEEA
LPTYQTMLDTLDGVRDETGASPTPWALMTRAWTAEENNHGDLLKKYLYLSGRVDMRQI
EXTIQVLLGSGMDPRTENSFYLGFIYTSFQERATFISHQNTARLARQHGDMKLAQICG
TIASDEKRHETAYTKIVEKLFEIDPOGTMLSLADMMKKVSVBPAHLMVDGHDBNLFEN
ESAVAQRIGVYTAKDVADILEHLIARWKVSDLTGLSGEGQKAQDYVCRLPPRIRKLEE
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255 c 315 g
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1319
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /EC_number="1.14.99.6"
/function="oleic acid synthesis"
/standard_name="delta-9 18:0-ACP
/codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="endosperm"
/clone_lib="lambda zapII cDNA expression library"
/dev_stage="postpollination"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Thunbergia alata"
/db_xref="taxon:32198"
/clone="pTAD1"
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Pred. No. 1.8e-117;
D; Mismatches 283;
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1 M83199.1 GI:169894

2 Stearoyl-acyl carrier protein desaturase.

2 Simmondsia chinensis embryo immature seed cDNA to mRNA.

2 Simmondsia chinensis

2 EUKATYOTA; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

2 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

2 Caryophyllidae; Caryophyllales; Simmondsiaceae; Simmondsia.

2 Caryophyllidae; Caryophyllales; Simmondsiaceae; Simmondsia.

3 (bases 1 to 1576)

3 LENCE 1 (bases 1 to 1576)

4 (bases 1 to 1576)

5 Sato,A.; Becker,C.K. and Knauf,V.C.

Nucleotide sequence of a complementary DNA clone encoding stearoyl-acyl carrier protein desaturase from Simmondsia chinensis stearoyl-acyl carrier protein desaturase from Simmondsia chinensis plant Physiol. 99, 362-363 (1992)

10 National Control of the Control of Control
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/product="stearoyl-acyl carrier protein desaturase"
/protein id="AAA33932.1"
/db_xref="GI:169895"
/tanslation="MALKLHHTAFNPSMAVTSSGLPRSYHLRSHRVFMASSTIGITSK
EIPNAKKPHMPPREAHVQKTHSMPPQKIEIFKSLEGWABENVLVHLKPVEKCWQPQDF
LPDPASEGFMDQVKELRERTKEIPDEYLVVLVGDMITEEALPTYQTMLNTLDGVRDET
                                                                                                                                                                                                                                              /organism="Simmondsia chinensis"
/db_xref="taxon:3999"
/tissue_type="immature seed"
/dev_stage="embryo"
                                                                                                                         /codon_start=1
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/EC_number="1.14.99.
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                                              GAAAAGCTCTTTGAAATCGACCCAGACGGCGCTGTTCTAGCACTAGCTGACATGATGAGA
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NPYLGFIYTSFQERATFISHGNTARLAKDHGDFQLAQVCGIIAADEKRHETAYTKIVE
KLFEIDPDGAVLALADMMRKKVSMPAHLMYDGKDDNLFENYSAVAQQIGVYTAKDYAD
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoides
                                                                                                                                                                                                                                                                                                                                 Tate, P.L., Kochert, G. and Abbott, A.G.
The phylogenetic relationship of the cultivated peanut (Arachis hypogaea L.) to its wild relative based upon comparisons of
                                                                                                                                                                                                                                                 Submitted (27-JUL-1999) Microbiology, SC 29634, USA
                                                                                                                                                                                                                                                                        Direct Submission
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Knauf, V.C. and Thompson, G.A.
Plant fatty acid synthases
Patent: US 5475099-A 32 12-DEC-1995;
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                                                                                 TIGACCGGCCTATCTGGTGAAGGGCGTAAAGCGCAAGATTATGTTTTGCGGGTTGCCACCA 1200
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          TCAGACGGATTCGAGGAGCAAGTGCGGGAGTTGAGGGAAAGGGCCCAAGGAGTTCCCGAC
                               GTTCACCTAAAGCCAGTGGAGAAATGTTGGCAAGCACAGGATTTCTTGCCGGACCCTGCA
                                                                       CCACCACAGAAGATAGAGATTTTCAAATCCATCGAGGGTTGGGCTGAGCAGAACATATTG
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Knauf, V.C. and Thompson, G.A.
Plant fatty acid synthases
Patent: US 5510255-A 32 23-APR-1996;
Location/Qualifiers
1. 1533
                                                                                                                                                                                                                                                                                                                                             Sequence
I19664
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Pred. No. 2.7e-116;
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                                       ACCGCCAAAGACTACGCCGACATACTGGAATTTCTGGTCGGGCGGTGGAAAGTGGCGGAT 1140
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CCTGTTTCTTCAGCTGGATTTTCAATCGGGAGTTGAAGATATGAACAGGAAGGGAAGG 1244
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Search completed: December Job time : 3492 secs 1, 2002, 23:59:59

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Maximum Match 100%
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

			Description
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	10	Q43141	sesamum
	10	Q9SEK6	a
	10	Q93X20	_
	10	Q39355	5 brassica
	10	024497	helianthu
	8	Q9XQR7	Q9xqr7 brassica ju
	10	Q9SW87	
	10	022832	
	10	Q94AE9	Q94ae9 arabidopsis
396	10	024498	
396	10	Q9M4N5	Q9m4n5 gossypium h
396	10	065040	065040 macfadyena
396	10	Q8S059	Q8s059 oryza sativ
358	10	Q43196	Q43196 thunbergia
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ر.	16	12	2	16	16	16	16	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10
Q26223	Q9x793	Q9WRP6	Q9K539	Q50824	Q8VKD4	Q50050	Q9XAL3	Q43142	Q9XFH1	064906	Q41510	P92933	Q40879	Q9MAR6	Q9M880	Q9xFC1	Q9LF05	Q9M881	Q947F2	Q9LF04	Q43198	Q42591	Q947F1	Q8VXJ7	Q8VXJ8	Q9M879	Q43197	Q9SBA2
plasmodium	Q9x793 mycobacteri	Q9wrp6 macaca mula	Q9k539 mycobacteri			_					_		Q40879 pelargonium						Q947f2 kochia scop						Q8vxj8 helianthus		Q43197 thunbergia	Q9sba2 linum usita

ALIGNMENTS

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RESULT 1
Q43140
    Q43140 PRELIMINARY; PRT; 396 AA. Q43140; Q1-140; Q1-14
                                          EMBL;
HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                     Plant Cell Physiol. 37:201-205(1996).

-: FUNCTION: CONVERTS STEARCYL-ACP TO OLECYL-ACP BY INTRODUCTION OF A CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL CHAIN (BY SIMILARITY).

-: CHAIN (BY SIMILARITY): STEARCYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)

-- OLECYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.

-- OLECYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96213006; PubMed=8665096;
Yukawa Y., Takaiwa F., Shoji K., Masuda K., Yamada K.;
"Structure and expression of two seed-specific cDNA clones encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sesamum indicum (Oriental sesame) (Gingelly).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesamum.
                                                                                                                   -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY
                                                                                                                                                                                                                                                                                                                                     +
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InterPro; IPR005067; FA_desat
                                                                                                                                                                                                                                                                                                                                PATHWAY:
                                                                                                                                                                                                                                                                                 PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY).
                                          D42086; BAA07681.1; P22337; 1AFR.
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Q43141;
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                                                                                                                                                                                                                               01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-JUN-2002 (TrEMBLrel. 21, 01-JUN-2002 (TrEMBLrel. 21, Acyl-[acyl-carrier protein] desaturase).
                                     Yukawa Y., Takaiwa F., Yamada K.;

"Structure and expression of two cDNA clones encoding st
carrier protein desaturase in sesame.";

Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INT
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10

CHAIN (BY SIMILARITY).

-i- CAPALLYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN]

- OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)0.

-i- COPACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AN
                                                                                                                                                                                        Sesamum indicum (Oriental sesame) (Gingelly).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core en
Asteridae; euasterids I; Lamiales; Pedaliaceae; Sesan
                                                                                                                                                STRAIN=4294;
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                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                             NCBI_TaxID=4182;
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                     SIMILARITY).

PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF VEGETABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                NRHGDLLNKYLYLSGRYDMRKIBKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISH
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QDYYCGLPPRIRRLEERAQGRAKQAP---KIPESWIHDREVQL
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            ACIDS
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pred. No. 4.2e-104;
pred. ---hes 57;
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TID ACCOMMENS OF THE PROPERTY 
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Best Local
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                                                                                                                Madd L., Prusky D.;

Madd L., Prusky D.;

"Sequence of a cDNA Clone Encoding an Idealizable Stearcyl-Acyl Carrier Protest Fills (1989) 167).";

AF116861). (PGR99-167).";

Plant physiol. 121:1054-1054(1999).

Plant physiol. 121:1054-2054(1999).

CIS DOUBLE BOND BETWEEN CARBONS DECISIONED DECISIONED TO COMPANY STEARCYL-ACP TO COMPANY STEARCYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D49832; BAA08635.1; --
HSSP; P22337; LAFR.
InterPro; IPR005067; FA_desaturase.
InterPro; IPR001225; FA_desaturase.
Pfam; PF03405; FA_desaturase_2; 1.
PROSTITE; PS00574; FATTY_ACID_DESATUR_2; 1.
Chloroplast; Fatty acid biosynthesis; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SUBUNIT: HOMODIMER (BY SIMILARITY)
-!- SUBCELLULAR LOCATION: CHLOROPLAST
-!- SIMILARITY: BELONGS TO THE FATTY AV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Transit
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Acyl-[acyl-carrier
desaturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Persea americana (Avocado).
Eukaryota; Viridiplantae; Streptophyta;
Spermatophyta; Magnoliophyta; Laurales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           237
                            CHAIN (BY SIMILARITY).

- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)0.

- OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                  STRAIN=CV. FUERTE;
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   COFACTOR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKA
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QDYVCGLPPRIRRLEERAQGRAKQAP---KIPFSWIHDREVQL
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279; Conservative
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         FERREDOXIN,
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            FERREDOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence update)
Last annotation update)
desaturase (EC 1.14.99.6) (Stearoy1-ACP
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Protein Desaturase (Ac
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No. 2
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DELTA-9 AND DI
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CID DESATURASE FAMILY
               NADPH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Embryophyta;
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               REDUCTASE,
                                                                                                                             PP BY INTRODUCTION OF DELTA-10 OF THE ACYL
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                  NADPH
                                                                           AH(2) + O(2)
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Best Local
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Stroyl acyl carrier protein.
Sesamum indicum (Oriental sesame) (Gingelly).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF116861; AAF15308.1; -.
HSSP; P22337; 1AFR.
InterPro; IPR005067; FA_desaturase.
InterPro; IPR001225; FA_desaturase.
Pfam; PF03405; FA_desaturase_2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2;
Chlorolic Desaturase_3; 1.
                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
Asteridae; euasterids I; Lamiales; Pedaliacea
                  TISSUE-DEVELOPING
Chopra V.L.;
                                                                      SEQUENCE FROM N.A
                                                                                                                  Submitted
                                                                                                                                    Kanrar S.;
                                                                                                                                                        TISSUE-DEVELOPING
                                                                                                                                                                               SEQUENCE FROM
                                                                                                                                                                                                                        NCBI_TaxID=4182;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q93X20
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    "Transgenic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
PATHWAY: CAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MALKLS-----PVMFQSQKLPFLASYPPSNLRSPRVFMASTLRSSTKEVDNIKKPFSP
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al Similarity 67.6%;
275; Conservative
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396 AA;
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  expression
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                                                                                                                                                                             N.A.
                                               SEED;
                                                                                                                                                        SEED;
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                                                                                                             EMBL/GenBank/DDBJ
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Pred. No. 7.
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Q39355;
01-NOV-1996 (TrEMBLrel. 01, 0
01-NOV-1996 (TrEMBLrel. 01, 1
01-JUN-2002 (TrEMBLrel. 21, 1
Acyl-[acyl-carrier protein] d
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Spermatophyta; Magnoliophyta;
eurosids II; Brassicales; Bras
                                                                                                                                                             BN4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-2001) to the EMBL; AJ313331; CAC44792.1;
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Submitted
                                                                                                                                                  Brassica napus
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                                                                                                            NCBI_TaxID=3708;
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                                                                                                                                                                                                                                                                                                                                                      GNTARLAREHGDLKLAQICGTIAADEKRHETAYTKIVEKLFEIDPNDTVLAFADMRKKI
                                                                                                                                                                                                                                                                                                                                                                 ANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKI
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                                                                                                                                                                                                                                                                             QDYVCGLPPRIRRLEERAQGRAKQAP---KIPFSWVHDREVQL
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                                                                                                                                                                                                                                                                                                                 SMPAHLMYDGRDDNLFDHFSSVAQRLGVYTAKDYADILEHLVARWKVANLTGLSADGQKA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VHVQVTHSMPPQKIEIFKALEDWADNNILVHLKPVEKCWQPQDFLPDPSSDGFDDQVKEL
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                                                                                                                      Brassicaceae;
                                                                                                                               Streptophyta; Embryorta; eudicotyledons;
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Last annotation update)
desaturase (EC 1.14.99.
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EMBL/GenBank/DDBJ
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               INTRODUCTION
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-: SUBCELLULAR LOCATION: CHLOR
-: SIMILARITY: BELONGS TO THE
EMBL; X74782; CAAS5786.1; --
HSSP; P22337; 1AFR.
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InterPro; IPR001225; FA_desaturase.
Pfam; PF03405; FA_desaturase2; 1.
PROSITE; PS00574; FAITY_ACID_DESATUR_2;
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                                                                                                                                                                                                                                                                 01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-JUN-2002 (TrEMBLrel. 21, Acyl-[acyl-carrier protein]
                                                                                                                                                                                                                                                                                                                                                                             024497;
                                                                                                                                                                                                                                                                                                                                                                                                      024497
                                 SEQUENCE
                                                                                                                                    Spermatophyta; Magnoliophyta; eudico Asteridae; euasterids II; Asterales;
                                                                                                                                                                                         Helianthus annuus (Common Eukaryota; Viridiplantae;
        STRAIN-MAMMOTH;
                                                                                   NCBI_TaxID=4232;
                                                                                                              Heliantheae;
                                                                                                                                                                                                                                              desaturase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MALKLNFQCKKNHPAAFAKSPLPVTRVSSPR-VFMAST----VNSNSMVLDNLKSP----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KEVHVQVLHSMPPQKIEIFKSMEDWAEQNLLTHLKDVEKSWQPQDFLPDPASDGFEDQVK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MALKLNPLASQPYKLPSSARP-PISTLRSPKFLCLASSSSPALSSSTKEVESLKKPFTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KAQEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KITMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLIGLSDEGR 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KAQEYLCGLTPRIRRLDERAQARAKKGP---KIPFSWIHDREVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SHGNTARQAKEHGDLKLAQICGTIAADEKRHETAYTKIVEKLLEIDPDGTVVAFADMMRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al Similarity 65.4
265; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            401
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                                                                                                              Helianthus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA;
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LOCATION: CHLOROPLAST (
BELONGS TO THE FATTY AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BETWEEN CARBONS DELTA-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45482 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               68.0%;
65.4%;
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                                                                                                                                                                                                                                              ., Created)
;, Last sequence update)
1, Last annotation update)
1. desaturase (EC 1.14.99.6
                                                                                                                                                                sunflower)
Streptophyta; Embry
yta; eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1401.5; Di
Pred. No. 8e-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1CCFB15626270401
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NADPH REDUCTASE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONVERSION OF SAI
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                                                                                                                                                                                                                                                                                                                                                                                                            396
                                                                                                                                             Asteraceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NADP; Oxidoreductase,
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                                                                                                                                                                   Embryophyta;
edons; core e
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DESATURASE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AND DELTA-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
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SIS OF VEGETABLE
                                                                                                                                                                                                                                                                            .6)
                                                                                                                                                                      eudicots;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FAMILY
                                                                                                                                                                                               Tracheophyta;
                                                                                                                                                                                                                                                                         (Stearoyl-ACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VEGETABLE
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RESULT
Q9XQR7
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 Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hongtrakul V., Slabaugh M.B., Knapp S.J.;
"Sunflower stearcyl-ACP desaturase.";
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
Submitted(FEB-1997) to the EMBL/GenBank/DDBJ databases.
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYLCIANIN (BY SIMILARITY).

CHAIN (BY SIMILARITY).

-I- CATALYTIC ACTILITY: STEAROYL-[ACYL-CARRIER PROTEIN] + A+ 2 H(2)0.

- OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)0.

- OLEOYL-SERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY COURTS).
Chloroplast.
Eukaryota; Viri
Spermatophyta;
                                                                                          Q9XQR7;
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; 091339; AAB65144.1;
HSSP; P22337; 1AFR.
InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
Pfam; PF03405; FA_desaturase_2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase; Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
                                                                  01-NOV-1999 (TREMBLIEL 01-NOV-1999 (TREMBLIEL 01-JUN-2002 (TREMBLIEL ACYL-[acyl-carrier prote
                                                                                                                            Q9XQR7
                                    Brassica
                                                          desaturase).
                                                                                                                                                                                                                                                                                                                                                                                              117
                                                                                                                                                                                                                                                                                                    237
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SUBCELLULAR LOCATION: CHLOROPLAST (BY
SIMILARITY: BELONGS TO THE FATTY ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACIDS TO UNSATURATED
                                                                                                                                                                                                                                                                                                                                                                                                                  ALRMSPVTLQREIYPSYTFHQSKNLRSPKFAMASTIGSSTPKVESTKKPFTPPREVHLQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AFAKSPLPVTR------PNLQV 56
                                                                                                                                                                                                                                                                                                                        EIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEENRHGD 176
                                                                                                                                                                                                                                                                             HAKDYGDLKLAQICGTIAADEKRHETAYTKIAEKLFEIDPDGTVLAFADMMRKKISMPAH
                                                                                                                                                                                                                                                                                        GLPSRIRRLEERAAARAK----
                                                                                                                                                                                                  ELGPKIRRVEEKVQGKEKKKKAEHP-VSFSWIFNRELKI
                                                                                                                                                                                                                                LMYDGRDDDLFDHFSAVAQRLGVYTAKDYADILEFLVGRWKVADLTGLSGEGRKAQDYVC
                                                                                                                                                                                                                                           LMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLYDKWNVERLTGLSDEGRKAQEYVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              al Similarity
267; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide.
396 AA;
                                 juncea (Leaf
 Viridiplantae; Str
yta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYZES
                                                                                                                              PRELIMINARY;
                                                                   BLrel. 12,
BLrel. 12,
BLrel. 21,
r protein]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45128 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         67.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              THE PRINCIPAL ED FATTY ACIDS
                                    mustard) (Indian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
               Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY
                                                                      Last sequence update)
Last annotation update)
desaturase (EC 1.14.99.
                                                                                                                                                                                      EGPSIPFSWIFDREVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1395; DB 10
Pred. No. 2.5e-99;
2; Mismatches 56
                                                                                                        Created)
                                                                                                                                PRT;
   eudicotyledons;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BC79CA9631952E11 CRC64;
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IN THE SYNT
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                                      mustard).
              Embryophyta;
                                                                                                                                AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY)
DESATURASE I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56;
                                                                                                                                                                                       396
      core
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length
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      eudi
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6)
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               Tracheophyta;
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                                                                        Stearoyl-ACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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RESULT
Q9SW87
ID Q9
AC Q9
DT 01
DT 01
DT 01
DT AC
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Best Local Similarity
Matches 266; Conserv
  Q9SW87;
Q9SW87;
01-MAY-2000
01-MAY-2000
01-JUN-2002
ACY1-(aCY1-ca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- SUBCELLULAR LOCATION: CHLOROPLAST (BY -1- SIMILARITY: BELONGS TO THE FATTY ACID EMBL; AF153420; AAD40245.1; -. HSSP; P22337; 1AFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transit |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Vageeshbabu H.S., Kirti P.B., Chopra V.L.;
"Nucleotide sequence of the coding region of the plastidic delta-9-stearoyl-acyl-acyl carrier protein desaturase of Brassica juncea.";
Submitted (MAX-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF CINCOLD BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chloroplast; Fatty acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR005067; FA_desat.
Interpro; IPR001225; FA_desaturase.
Pfam; PF03405; FA_desaturase_2; 1.
PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           eurosids II; Brassicales;
NCBI_TaxID=3707;
                                                                                                                                                                        345
                                                                                                                                                                                                                                                           235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN (BY SIMILARITY).

CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] +

OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.

COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).

PATHWAY: CATALYZES THE PRINCIPAL ACIDS TO UNSATURATED FATTY ACIDS
                                                                                                                                                                                                                                                       RATFISHANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFA 284
                                                                                                                                         SGEGNKAQEYLCGLTPRIRRLDERAQARAKKGP---KIPFSWIHDREVQL
                                                                                                                                                         SDEGRKAQEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI 394
                                                                                                                                                                                                 DMMRKKITMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGL 344
                                                                                                                                                                                                                                                                                                              RAWTAEENRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENNPYLGFIYTSFQE
                                                                                                                                                                                                                                                                                                                             RAWTAEENRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQE
                                                                                                                                                                                                                                                                                                                                                                                     EEQVRELRERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWT 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                           P----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MALKLNPLASQPYNFPSSARPPISTFRSPKFLCLASSSSP-----ALSSSTKEVESLKK 54
X'-2000 (TrEMBLrel. 13, Created)
X'-2000 (TrEMBLrel. 13, Last sequence update)
N'-2002 (TrEMBLrel. 21, Last annotation update)
[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACF)
                                                                                                                                                                                                                                                                                                                                                                    EDQVKELRERARELPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTPWAVWT
                                                                                                                                                                                                                                                                                                                                                                                                                           PFTPPKEVHVQVLHSMPPQKIEIFKSMEDWAEQNLLTHLKDVEKSWQPQDFLPDPASDGF 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide.
E 401 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         -PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGF 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JAIKISAN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                       PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 45504 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        67.5%;
64.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1391.5; DB Pred. No. 4.7e-99;
                                                                         PRT;
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IN THE SYNT
                                                                         409
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VEGETABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AH(2) + O(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                    174
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RESULT 9
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SUBUNIT: HOMODIMER (BY SIMILARITY).
-!- SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
EMBL; AF172728; AAD48495.1; -.
HSSP; P2337; 1AFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
Pfam; PF03405; FA_desaturase_2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hypogaea L.) to its wild relative based upon comparisons of stearo ACP desaturase sequences.";
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION CIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arachis hypogaea (Peanut).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
022832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chloroplast; Fatty acid biosynthesis; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transit peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tate P.L., Kochert G., Abbott A.G.;
"The phylogenetic relationship of the cultivated peanut
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arachis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eurosids I; Fabales; Fabaceae; Papilionoideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3818
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                                                            361
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CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + CAEOXL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.

COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PATHWAY: CATALYZES THE PRINCIPAL ACIDS TO UNSATURATED FATTY ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY).
                                                        MALKLN-----FQCKKNHPAAFAKS-PLP-VTRVSSPRVEMASTVNSNSMYLDNLKSP
                                                                                                                                                                                                                        AWTAEENRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQER
                                                                                                                                                                                                                                                                       EQVRELRERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAWWTR 165
                                                                                                                                                                                                                                                                                                          FTPPREVHVQGNHSMPPQKIEIFKSLEGWAEENILTLLKPVEKCWQPQDYLPEPSEDGFE
                                                                                                                                                                                                                                                                                                                             -----PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFE
                                                                                                                                                                                                                                                                                                                                                           MALRINPNPSQKLFLSPSSSSSSSSSSSSFSLPQMASLRSPRFRMASTLRTGSKEVENLKKP
                                                                                                                                                                                                            AWTAEENRHGDLLNKYLYLSGRVDLRQIEKTIQYLIGSGMDPRTENSPYLGFIYTSFQER
                                                                                                                                                                                                                                                            EQVRELRARAKELPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTSWAVWTR
                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           409 AA;
PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           46810 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                       67.1%;
66.3%;
                                                                                                                                                                                                                                                                                                                                                                                                            51;
                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1384.5;
Pred. No. 1.7
PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           7C80926BD8534A58 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CONVERSION OF SATURATED FATTY IN THE SYNTHESIS OF VEGETABLE
401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Embryophyta; Tracheophyta;
edons; core eudicots; Rosid
AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oxidoreductase,
                                                                                                                                                                                                                                                                                                                                                                                                            65;
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                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of stearoyl-
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                                                                                                                                                                                                                                                                                                                                                                                                                                   409;
                                                            409
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Best Local
                                                                                                             Matches
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                                                                                                                                                                                                                                                               -!- SUBUNIT: HOMODIMER (BY SIMI
-!- SUBCELLULAR LOCATION: CHLOR
-!- SIMILARITY: BELONGS TO THE
EMBL; AC002333; AAB64035.1; --
EMBL; AF395441; AAK85232.1; --
HSSP; P22337; 1AFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=21374454;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-car cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core «
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JAN-1998 (TIEMBLIEL 05, 01-JAN-1998 (TIEMBLIEL 05, 01-JUN-2002 (TIEMBLIEL 21, Acyl-[acyl-carrier protein]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=21374454; PubMed=11481500;
Kachroo P., Shanklin J., Shah J., Whittle E.J., Klessig D.F.,
"A fatty acid desaturase modulates the activation of defense
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=3702;
                                                                                                                                                                                            Chloroplast; Fatty acid biosynthesis;
                                                                                                                                                                                                            PROSITE;
                                                                                                                                                                                                                          Pfam; PF03405;
                                                                                                                                                                                                                                    InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
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60
                           52
                                                                                 \vdash
                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN (BY SIMILARITY).

CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] +

OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.

COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND
                                                                                                                                                                                                                                                                                                                                                                ACIDS
                                                                                                                                                                                                                                                                                                                                                                              PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                           SIMILARITY).
                                                                    MALKLNFQCKKNHPAAFAKSPLPVT-RVSSPR-VFMAST---VNSNSMVLDNLKSP----
 REVHVQVLHSMPPQKIEIFKSMENWAEENLLIHLKDVEKSWQPQDFLPDPASDGFEDQVR
                         --PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVR
                                                      MALKFN-PLVASQPYKFPSSTRPPTPSFRSPKFLCLASSSPALSSGPKEVESLKKPFTPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        402:761-768(1999).
                                                                                                                          Similarity
                                                                                                                                                                               peptide.
                                                                                                                                                                                                          03405; FA_desaturase_2; 1.
PS00574; FATTY_ACID_DESATUR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FROM N.A.
                                                                                                                                                                                                                                                                                                                                                             AY: CATALYZES THE PRINCIPAL TO UNSATURATED FATTY ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MAR-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COLUMBIA;
                                                                                                                                                                                                                                                                                                                                    HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.A.
                                                                                                                                                                   AA;
                                                                                                                                                                   45693 MW;
                                                                                                                        67.0%;
                                                                                                                                                                                                                                                                                                         CHLOROPLAST (BY SIMILARITY)
O THE FATTY ACID DESATURASE
                                                                                                             61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
desaturase (EC 1.14.99.6)
                                                                                                                       Score 1381.5;
Pred. No. 2.8
                                                                                                                                                                  0C46984578D4E1D1 CRC64;
                                                                                                             Mismatches
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edons; core eudicots; Rosidae;
                                                                                                                          8e-98
                                                                                                                                                                                                                                                                                                         DESATURASE FAMILY
                                                                                                                                       DB 10;
                                                                                                                                                                                            Oxidoreductase;
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                                                                                                                                     Length
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Query Ma
Best Loc
Matches
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Koesema E., CIC
- T., Bowser I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koesema E., Chen H., Cheuk R., Kim C.J., Meyers M.C., Shinn P., Banh J., Bowser L., Carninci P., Dale J.M., Gibson H.A., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J. Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick Tang C.C., Toriumi M., Yamada K., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
"Arabidopsis CDNA Clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
01-DEC-2002 (TrEMBLrel. 21, Last annotation update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
01-DEC-2001 (TrEMBLrel. 21, Last annotation update)
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 
                                                                                                                                                                                                                         "Arabidopsis ORF clones.";
Submitted (APR-2002) to the
EMBL; AY048233; AAK82496.1;
EMBL; AY094014; AAM16170.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Cheuk R., Chen H., Kim C.J., Meyers M.C., Shinn P., Banh J., Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith-Neumann Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
                                                                                                 InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
Pfam; PF03405; FA_desaturase_2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2; UNKNOWN 1.
SEQUENCE 401 AA; 45692 MW; 01F09DD370F4E1D1 CR
                                                                                                                                                                                                                                                                                                                                                                                    Nguyen M.,
Seki M., S
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  266;
                                                                                                                                                                                                                                                                                                                                   J.R.;
                          Similarity
                                                                                                                                                                                                                                                                                                                                                        Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Sa
Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada I
Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis
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  Conservative
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                            67.0%;
65.7%;
  61;
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                            Pred.
                                                 Score
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  Mismatches
                            1381.5;
No. 2.8e
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     63;
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  Indels
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                                               Length
     15;
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  Gaps
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MALKLNFQCKKNHPAAFAKSPLPVT-RVSSPR-VFMAST--

-VNSNSMVLDNLKSP-

ОУ

52

--PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVR

109

MALKEN-PLVASQPYKEPSSTRPPTPSERSPKFLCLASSSPALSSGPKEVESLKKPFTPP

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NEW WELL BORREST CONTRACTOR OF THE CONTRACTOR OF
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  Query Match
Best Local
                                                                   Transit p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Helianthus annuus (Common sunflower).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Asteridae; euasterids II; Asterales; Asteraceae; Aste
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01-JAN-1998 (TrEMBLrel. 05,
01-JAN-1998 (TrEMBLrel. 05,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                       Chloroplast; Fatty
                                                                                                                                 Pfam; PF03405; FA_desaturase_2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2;
                                                                                                                                                                             InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
                                                                                                                                                                                                                         EMBL; U91340; AAB65145.1; HSSP; P22337; 1AFR.
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                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN (BY SIMILARITY).

CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] +

OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)0.

COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND
                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                      PATHWAY:
                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                            ACIDS
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||||||:::||:||:||:||:||
ELRERARELPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTA
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  Similarity
                                                                                     peptide.
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                                                                   396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                 CATALYZES
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                                                                   ΑĄ;
                                                                                                            acid biosynthesis;
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                                                                   45112 MW;
  67
66
                                                                                                                                                                                                                                                                  (BY SIMILARITY).

ON: CHLOROPLAST (BY
S TO THE FATTY ACID
                                                                                                                                                                                                                                                                                                                                                            THE PRINCIPAL ED FATTY ACIDS
  . 5%;
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Last annotation update)
desaturase (EC 1.14.99.6)
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Score
Pred.
                                                                   C9D88CD04310BBFA CRC64;
                                                                                                                                                                                                                                                                                                                                                          ACIDS
NO.
                                                                                                                                                                                                                                                                                                                                                     CONVERSION OF SAY
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                                                                                                            NADP;
1; DB
3e-98;
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                                                                                                                                                                                                                                                                                         SIMILARITY)
                                                                                                                                                                                                                                                                     DESATURASE
                                                                                                          Oxidoreductase;
                    10;
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                    Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   eudicots;
                                                                                                                                                                                                                                                                                                                                                                                 SATURATED FATTY
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                         396;
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9M4N5;
        InterPro; IPRO05067; FA_desat.
InterPro; IPRO01225; FA_desaturase.
Pfam; PF03405; FA_desaturase_2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2;
                                                     -:- SUBUNIT: HOMODIMER (BY SIMILARITY)
-:- SUBCELLULAR LOCATION: CHLOROPLAST
-:- SIMILARITY: BELONGS TO THE FATTY &
EMBL; AJ132636; CAB75356.1; -.
HSSP; P22337; 1AFR.
                                                                                                                                                                                                                                Submitted (FEB-1999)
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Strepto
Spermatophyta; Magnoliophyta; eud
eurosids II; Malvales; Malvaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-2000 (TrEMBLrel. 15, 01-OCT-2000 (TrEMBLrel. 15, 01-JUN-2002 (TrEMBLrel. 21, Acyl-[acyl-garrier protein]
                                                                                                                                                                            CHAIN (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] +

-i- CATALYTIC ACTIVITY: ARRIER PROTEIN] + A + 2 H(2)0.
                                                                                                                                              <del>-</del>
                                                                                                                                                                      <del>'</del>
                                                                                                                                                                                                                                                         cotton."
                                                                                                                                                                                                                                                                                             STRAIN-CV.
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                Gossypium hirsutum (Upland cotton)
                                                                                                                                                                                                                                                                                                                                                                                              SAD1.
                                                                                                                                                                                                                                                                                 Liu Q., Singh S., Green A.;
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3635;
                                                                                                                                                                                                                                                                   "Genomic Organisation of AE9 stearoyl-ACP desaturase
                                                                                                                                                                                                                                                                                                                                                                                                        (Stearoyl-ACP desaturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172
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                                                                                                                                 PATHWAY:
ACIDS TO
                                                                                                                                                                   = OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2
COFACTOR: FERREDOXIN, FERREDOXIN NADPH
                                                                                                                                                                                                                    FUNCTION: CONVERTS STEAROYL-ACP CIS DOUBLE BOND BETWEEN CARBONS
                                                                                                                                                          SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNTARHAKEHGDVKLAQMCGIIAADEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MALKLN---FQCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QDYVCGLAPRIRRLEERNSARAKESV---NVPFSWIFDREVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMPAHLMYDGRDDNLFENFSAVAQRLGVYTAKDYADILEFLVGRWKVADLTGLSGEGRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VHQQVLHSMPPQKIEIFKSMEGWAEDNILVHLKPVEKCWQAQDFLPDPASDGFMEQVEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAIRINTATEQSDLYRSFAFPQ-PKP---LRSPKFAMASTIGSATTKVESTKKPETPPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        268;
                                                                                                                                                                                                                                                                                             DELTAPINE-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                 CATALYZES THE PRINCIPAL UNSATURATED FATTY ACIDS
Fatty acid biosynthesis;
                                                                                                          HOMODIMER (BY SIMILARITY)
                                                                                                                                                                                                                                  to the EMBL/GenBank/DDBJ
TS STEAROYL-ACP TO OLEOYL
                                                                                                                                                                                                                                                                                                                                                       Streptophyta; Embry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54;
                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
desaturase precursor (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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DELTA-9 AND DE
                                                                                  ACID
                                                                                                                                 CONVERSION OF
IN THE SYNTHES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                396
NADP;
                                                                                               (BY
                                                                                                                                                                                                                                                                                                                                                                   Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
                                                                                 SIMILARITY)
DESATURASE
                                                                                                                                                                     REDUCTASE,
Oxidoreductase;
                                                                                                                                  SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65;
                                                                                                                                                                                                                                             databases
                                                                                                                                                                                                                                                                                                                                                         core
                                                                                                                                                                                                                     DELTA-10
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                                                                                                                                                                                                                                  BY INTRODUCTION
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                                                                                                                                               SATURATED FATTY
                                                                                                                                                                                                                                                                                                                                                         eudicots;
                                                                                  FAMILY
                                                                                                                                                                                                                                                                    genes
                                                                                                                                  OF.
                                                                                                                                                                      AND
                                                                                                                                 VEGETABLE
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                                                                                                                                                                      NADPH
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                                                                                                                                                                                                                     THE ACYL
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6
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Matches 273
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TRANSIT
CHAIN
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                                                                                                                                                                                                                                      FADI.
Macfadyena unguis-cati.
Macfadyena unguis-cati.
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core et
Spermatophyta; Magnoliophyta; Bignoniaceae; Mac;
                                                                                                                                                                                                                                                                                                FAD1
                                                                                                                                                                                                                                                                                                                    01-AUG-1998 (TrEMBLrel. 07, 01-AUG-1998 (TrEMBLrel. 07, 01-JUN-2002 (TrEMBLrel. 21, Acyl-{acyl-carrier protein}
                                                                                                                                                                                                                                                                                                                                                                               065040
                                                                                                                                                     Desaturase of Developing Doxantha Seplant Physiol. 0:0-0(1998).
-i- FUNCTION: CONVERTS STEAROYL-ACP
                                                                                                                                                                                                                                   Asteridae; euasterids
NCBI_TaxID=73871;
 EMBL;
                                                                                                                                                                             Cahoon E.B., Shah S., Shanklin J., Browse J.;
"A Determinant of Substrate Specificity Predicted Desaturase of Developing Doxantha Seed.";
                                                                                                                                                                                                                                                                                                           desaturase).
                                                                                                                   <del>'</del>-
                                                                                                                                                                                                                 SEQUENCE
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                                                                                        CHAIN (BY SIMILARITY).

CHAIN (BY SIMILARITY).

CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN]

- OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.

COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AN
ACIDS TO UNSATURATED FATTY ACIDS IN THOLIS.
OILS.
SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CHLOROPLAST (BY
SIMILARITY: BELONGS TO THE FATTY ACID
L; AF051134; AAC05293.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALKLNFQCKKNHP-AAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLK---SPDN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MALNENAIASKSQKLPCFALPPKATLR--SPKFSMISTIPSGSKEVGNLKKPFTPPKEVP
                                                                                  SIMILARITY)
                                                                                                                                           CIS DOUBLE BOND BETWEEN CARBONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAKEIPDDYFVVLVGDMITEEALSTYQTMLNTLDGTRDETGASLTPWAIWTRAWTAEENR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEENR
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396
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                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                       CATALYZES
                                                                                                                                                                                                                 N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32
396
45188
                                                                       THE
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                                                            HE PRINCIPAL FATTY ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1377; Di
Pred. No. 6.1e:
10; Mismatches
                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation updat
desaturase (EC 1.14.9
                                                                                                                                                                                                                                                                                                                                                          Created)
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AE9 STEAROYL-ACP DESATURASE
9F61C35A7363D9AB CRC64;
                                                                                                                                            TO OLEOYL-ACP
DELTA-9 AND DE
                                                           CONVERSION OF SATURATED FATTY IN THE SYNTHESIS OF VEGETABLE
                                                                                                                                                                                                                                                                                                                                                                                 396
              (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                      ation update)
(EC 1.14.99.6)
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6.1e-98;
hes 76;
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                                                                                                                                            CP BY INTRODUCTION DELTA-10 OF THE AC
                                                                                                                                                                                                                                                    re eudicots;
Macfadyena.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                           from
                                                                                                                                                                                                                                                                          Tracheophyta;
                FAMILY
                                                                                                 AND
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                                                                                                                                                                                            the
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                                                                                                                      AH(2)
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                                                                                                                       0(2)
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OR CONTROL OF CON
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Best Loc
Matches
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Best Local Similarity
Matches 256; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HSSP; P22337; 1AFR.
InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
Pfam; PF03405; FA_desaturase_2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
Chloroplast; Fatty acid biosynthesis; NADP; Oxidoreductase;
Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q8S059 PRELIMINARY; PRT; 396 AA. Q8S059; O1-JUN-2002 (TrEMBLrel. 21, Created) O1-JUN-2002 (TrEMBLrel. 21, Last sequence up O1-JUN-2002 (TrEMBLrel. 21, Last annotation putative stearcy1-acy1-carrier protein desat P0678F11.19. Oryza sativa (japonica cultivar-group) Oryza sativa (japonica cultivar-group)
                                                                                                                                                                                                                                                               EMBL; APO
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oryza sativa (japonica cultivar-group). Eukaryota; Viridiplantae; Streptophyta; En Spermatophyta; Magnoliophyta; Liliopsida; Ehrhartoideae; Oryzeae; Oryza. NCBI_TaxID=39947;
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                                                                                                                                                                                                                                                                                             "Oryza sativa nipponbare(GA3) genomic DNA, chr clone:p0678F11."; clone:p0678F11."; submitted (MAR-2001) to the EMBL/GenBank/DDBJ EMBL; AP003437; BAB86112.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=CV. NIPPONBARE Sasaki T., Matsumoto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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RYYAVAS-GAVSTKVENKKPFAPPREVHVQVTHSMPPQKIEIFKSLDDWARDNILSHLKP
                                          RVFMASTVNSNSMYLDNIK--SPP---NLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKS
                                                                                                                                                                                                                                                                                                                                                                                     =CV. NIPPONBARE;
T., Matsumoto T., Yamar
sativa nipponbare(GA3)
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Pred. No. 1
                                                                                                                                         Score 1370.5;
Pred. No. 1.9e
53; Mismatches
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.8e-97;
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a; Poales; Poaceae;
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..9e-97;
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   Query Match
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Acyl-[acyl-carrier protein] desaturase (EC 1.14.99.6) (Stearoyl-ACI desaturase) (Fragment).
Thumbergia alata (black-eyed Susan vine).
Enkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Acanthaceae; Thumbergia.
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Q43196;
                                                 Transit
                                                                        EMBL; U07552; AAA61558.1; -.
HSSP; P22337; 1AFR.
InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
Pfam; PF03405; FA_desaturase.2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
CCLOCOPLAST; Fatty acid biosynthesis; NADP;
                                                                                                                                                                                                                                                                                                                                                        Plant Physiol. 106:807-808(1994).
-!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95083771; PubMed=7991701;
Cahoon E.B., Becker C.K., Shanklin J., Ohlrogge J.B.;
"cDNAs for isoforms of the delta 9-stearcyl-acyl carrier protein desaturase from Thunbergia alata endosperm.";
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                                                                                                                                                                                    SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CHLOROPLAST (BY SIMILARITY).
SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY
                                                                                                                                                                                                                                                                                             CHAIN (BY SIMILARITY).

CATALYTIC ACTIVITY: STEAROYL-[ACYL-CARRIER PROTEIN] + AH(2) + O(2)

- OLEOYL-[ACYL-CARRIER PROTEIN] + A + 2 H(2)O.

COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH (BY
                                                                                                                                                                                                                                             SIMILARITY).

PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
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01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acyl-[acyl-carrier protein] desaturase, chloroplast
(EC 1.14.99.6) (Stearoyl-ACP desaturase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-91172837; PubMed=2006187; Shanklin J., Somerville C.R.; Starcyl-acyl-carrier-protein desaturase from higher plants structurally unrelated to the animal and fungal homologs."; proc. Natl. Acad. Sci. U.S.A. 88:2510-2514(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   carrier protein desaturase).
Ricinus communis (Castor bean).
Ricinus communis (Castor bean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Epermatophyta; Magnoliophyta; eudicotyledons; core expermatophyta; Magnoliophyta; Euphorbiaceae; Ricinus.
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                                             MEDLINE-97015109; PubMed-8861937;

MEDLINE-97015109; PubMed-8861937;

Lindqyist Y., Huang W., Schneider G., Shanklin J.;

Lindqyist Y., Huang W., Schneider G., Shanklin J.;

"Crystal structure of delta9 stearcyl-acyl carrier protein

from castor seed and its relationship to other di-iron prot

EMBO J. 15:4081-4092(1996).

-I- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTROL

-I- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTROL

-I- GUNGTION: CONVERTS STEAROYL-ACP BY INTROL

-I- 
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                                                                                                                                                                                                                                                                                                                                    Knutzon D.S., Scherer D.E., Schreckengost W. "Nucleotide sequence of a complementary DNA acyl carrier protein desaturase from castor plant Physiol. 96:344-345(1991).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ELRERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPPNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVR 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD;
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- oleoyl-[acyl-carrier protein] + A + 2 H(2)0.
-!- COFACTOR: FERREDOXIN, FERREDOXIN MADDH REDUCTASE, AND
-!- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURAT
ACIDS TO UNSATURATED FAITY ACIDS IN THE SYNTHESIS OF V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content use by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S16463; OHCSAD.
PIR; A39170; A39170.
PDB; 1AFR; 15-MAY-97.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for entities requires a license agreement (Sce http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                            Transit peptide; 3D-structure.
TRANSIT 1 33 C
CHAIN 34 396 F
                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001225; FA_desaturase.

Pfam; PF03405; FA_desaturase_2; 1.

PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1

Oxidoreductase; Fatty_acid_biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; X56508;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M59857;
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase
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SIMILARITY: BELO
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                                                                                                                                                                                                                                     MALKLNPFLSQTQKLPSFALPPMASTR--SPKFYMASTLKSGSKEVENLKKPFMPPREVH
                                                                                                                                       TAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKITM
                                                                                                                                                                                        RAKEIPDDYFYVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAEENR
                                                                                                                                                                                                    RAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEENR 173
                    YVCELGPKIRRVEEKVQGKEKKKKAEHP-VSFSWIFNRELKI
                                            PAHLMYDGRDDNLFDHFSAVAQRLGVYTAKDYADILEFLVGRWKVDKLTGLSAEGQKAQD
                                                       PAHLMYDGSDELLEKHETAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKAQE
YVCRLPPRIRRLEERAQGRAK----
                                                                                                                                                                                                                                                                                                                                    286;
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71.1%;
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                                                                                                                                                                                                                                                                                                                                                Score 1490; DB 1
Pred. No. 5e-103;
                                                                                                                                                                                                                                                                                                                                                                                   ACYL-[ACYL-CARRIER PROTEIN] DESATURASE; E50D4725996392AF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                            CHLOROPLAST (BY SIMILARITY)
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15-JUN-2002 (Rel. 41, Last annotation update)
Acyl-lacyl-carrier protein] desaturase, chloroplast precursor (EC 1.14.99.6) (Stearoyl-ACP desaturase).
                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                         CHAIN
                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF03405; FA_desaturase_2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L34346; AAA92462.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Glycine
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15-DEC-1998 (Rel. 37,
15-JUN-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      HSSP; P22337;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3847;
                 227
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COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SAT ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PINONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FUNCTION: CONVERTS STEAROYL-ACP CIS DOUBLE BOND BETWEEN CARBONS
                                                                                                                                                                                                                                     MALKLNFQCKKNHPAAFAKSPLPVTRVS-----SPRVFMASTVNSNSMVLDNLKSP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EN
European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Gene Register PGR95-105.
                                                                                               TFISHANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADM
                                                      WTAEENRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERA
                                                                                                                                                      TPPREVHVQVTHSMPPQKIEIFQSLEDWAEENILAHLKPVEKCWQPQDFLPDPSSDGFEE
                                                                                                                                                                    -----PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEE 106
                                           WTAEENRHGDLLNKYLYLSGRVDMKQIEKTIQYLIGSGMDPRTENSPYLGFIYTSFQERA
                                                                                                                            QVRELRERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  g and sequence of a cDNA encoding
desaturase from Glycine max.";
                                                                                                                                                                                                                                                                                                                                                                   peptide.
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                                                                                                                                                                                                                                                                                                                         411 AA;
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67.7%;
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                                                                                                                                                                                                             PIPTQTFSLPQMASLRSPRFRMASTLRSGSKEVENIKKPF
                                                                                                                                                                                                                                                                                                                           MW;
                                                                                                                                                                                                                                                                    46;
                                                                                                                                                                                                                                                                                 Score 1422.5;
Pred. No. 5.2
                                                                                                                                                                                                                                                                                                                         ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.; 2727C3EDC8C97BA8 CRC64;
                                                                                                                                                                                                                                                                                                                                                     CHLOROPLAST (BY SIMILARITY)
                                                                                                                                                                                                                                                                    Mismatches
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DELTA-9 AND DE
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                                                                                                                                                                                                                                                                                  2e-98;
                                                                                                                                                                                                                                                                                              DB 1;
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                                                                                                                                                                                                                                                                                            Length 411;
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SIS OF VEGETABLE
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RESULT 4
STAD_CUCSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Shanklin J., Mullins C., Common Cu
Sequence of a complementary DNA from Cu
"Sequence of a complementary DNA from Cu
stearoyl-acyl-carier protein desaturase.
plant Physiol. 97:467-468(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acyl-[acyl-carrier protein] desaturase, chloroplast precursor (EC 1.14.99.6) (Stearoyl-ACP desaturase).

Cucumis sativus (Cucumber).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheop
                            Transit
TRANSIT
                                                                                                                                 EMBL; M59858; AAA33130.1;
PIR; B39170; B39170.
HSSP; P22337; 1AFR.
                                                                                                                                                                                      was by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Stearoyl-acyl-carrier-protein desaturase from higher plants structurally unrelated to the animal and fungal homologs."; Proc. Natl. Acad. Sci. U.S.A. 88:2510-2514(1991).
-i- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION: CONVERTS STEAROYL-BY TO OLEOYL-ACP BY INTRODUCTION: ONLY STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core evenosids I; Cucurbitales; Cucurbitaceae; Cucumis.
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    CONFLICT
                                                           Oxidoreductase;
                                                                         PROSITE;
                                                                                                    InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
                                                                                                                                                                                                                                                                  between
                                                                                                                                                                                                                                                                                                                                                                                                                             -i- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier p oleovl-[acyl-carrier protein] + A + 2 H(2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shanklin J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Seedling
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=3659;
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                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                 = oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE,
PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SAY
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS
                                                                                                                                                                                                                                                                                                       NONPHOTOSYNTHETIC TISSUES.
SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                        SUBUNIT: HOMODIMER (BY SIMILARITY)
SUBCELLULAR LOCATION: CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MRKKITMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSD
                                                                  PF03405; FA_desaturase_2; 1.
TE: pS00574; FATTY_ACID_DESATUR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGRKAQEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRE
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                                         peptide.
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Mullins C., S
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                                                        Fatty acid
 33
396
114
                                                                                                                                                            .'
                                                        biosynthesis;
CHLOROPLAST (BY SIMILARITY).

ACYL-[ACYL-CARRIER PROTEIN] DESATURASE
R -> V (IN REF. 2).
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                                                         NADP; Chloroplast
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                                                                                                                                                                                                                                                                                                                                                                                    SYNTHESIS
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p28645;
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acyl-[acyl-carrier protein] desaturase, chloroplast
(EC 1.14.99.6) (Stearoyl-ACP desaturase).
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-cv. Biroflea; TISSUE-Cotyledon;
MEDLINE-92329733; PubMed-1627785;
Beppu T., Nishida I., Matsuo T., Murata N.;
Beppu T., Nishida I., Matsuo T., Murata N.;
"Nucleotide sequence of a cDNA clone encoding a "Nucleotide sequence of a cDNA clone encoding a "Nucleotide sequence of a cDNA clone encoding a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spinacia oleracea (Spinach).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;

Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
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                                                                                                                                                                                                                                                                                                                                                                             stearoyl-(acyl-carrier-protein) desaturase
oleracea.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3562;
                                                                                                                                                                                                                                                                                                                                                Plant Mol. Biol. 19:711-713(1992)
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                                                                                                                                             CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + Ceoyl-[acyl-carrier protein] + A + 2 H(2)O.

COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.

PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY

ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
                                                                                                                                                                                                                                                                                                    FUNCTION: CONVERTS STEAROYL-ACP CIS DOUBLE BOND BETWEEN CARBONS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MALKF------HPLTSQSPKLPSFRMPQLASLRSPKFVMASTLRSTSREVETLKKPFMP
                       NONPHOTOSYNTHETIC TI
SIMILARITY: BELONGS
                                                                         SUBCELLULAR LOCATION:
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45583 MW;
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                          TO THE FATTY ACID DESATURASE FAMILY
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.9e-97;
                                                                                GREEN TISSUE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X62898; CAA44687.1; -.

PIR; S22480; OHSPAD.

HSSP; P22337; 1AFR.

InterPro; IPR005067; FA_desat.

InterPro; IPR001225; FA_desaturase.

InterPro; IPR001225; FA_desaturase.

Pfam; PF03405; FA_desaturase_2; 1.

PROSITE; PS00574; FATTY_ACID_DESATUR_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transit peptide.
TRANSIT 1
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                                                                                                                                                                                                                                 STAD_CARTI STANDARD; PRT; 396 AA. p22243; p222
                                                                                                                                                                                                                                                                                                                                                                                                     CARTI
                                                                                                                                                       Carthamus tinctorius (Safflower).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core el
Spermatophyta; Magnoliophyta; eudicotyledons; core el
  MEDLINE=91172850; PubMed=2006194; Thompson G.A., Scherer D.E., Foxa
                                                                                                              Asteridae; euasterids
NCBI_TaxID=4222;
                                                                       SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             177
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273; Conserv
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45663 MW;
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67.2%;
                                                                       PARTIAL SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1410.5; DB 1; pred. No. 3.8e-97; 9; Mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACYL-[ACYL-CARRIER PROTEIN] DESATURASE; 59B56E0609EA7CCC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHLOROPLAST
       Foxall-Van
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                Asteraceae;
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         Aken
         s.
                                                                                                                                                  core eudicots;
le; Cardueae; (
         Kenny
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                                                                                                                                                                                                                                                                   precursor
                                                                                                                                                                                               Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19;
                                                                                                                                                     Carthamus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Best Local Similarity
Matches 271; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
MOD_RES
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Stearoy1-acy1 Carrie Freedoxin for enzyme activity.";
requirement of ferredoxin for enzyme activity.";
Proc. Natl. Acad. Sci. U.S. A. 88:2578-2582(1991).
-1- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION CF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR005067; FA_desaturase.
InterPro; IPR001225; FA_desaturase.
Pfam; PF03405; FA_desaturase_2; 1.
PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; M61109; AAA33021.1; -. PIR; A39173; A39173. HSSP; P22337; LAFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         between the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Primary structures of the precursor and mature forms of stearoyl-acyl carrier protein desaturase from safflower embryos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Transit
 357
                               352
                                                                                         292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oleoyl-[acyl-carrier protein] + A + 2 H(2)O.
COPACTOR: FERREDOXIN, FERREDOXIN NADPRESION OF SATURATED
PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] +
    oleoyl-[acyl-carrier protein] + A + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: CHLOROPLAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NONPHOTOSYNTHETIC TISSUES
                                                                                                                                                                                                                                                                                                MALKL---NFQCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
QDYVCGLPPRIRRLEERAQGRAK - - -
                                                                        TMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKA 351
                                                                                                                                                ANTAKLAOHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKI
                                                                                                                                                                                             NRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISH
                                                                                                                                                                                                                                                                                                                 PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVREL
                                                                                                                                                                                                                                                                                                                                                             MALRITPVTLQSERYRSFSFPKK----ANLRSPKFAMASTLGSSTPKVDNAKKPFQPPRE
                            QEYVCELGPKIRRVEEKVQGKEKKKKAEHP-VSFSWIFNRELKI
                                                        SMPAHLMYDGRDDNLFEHFSAVAQRLGVYTAKDYADILEFLVGRWKVADLTGLSGEGRKA
                                                                                                                   GNTARHAKDHGDVKLAQICGTIASDEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKI
                                                                                                                                                                                                                                       RARAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTPWAVWTRAWTAEE
                                                                                                                                                                                                                                                        RERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEE
                                                                                                                                                                            NRHGDLLHTYLYLSGRVDMRQIQKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFVSH
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396
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396
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                                                                                                                                                                                                                                                                                                                                                                                                                     Score 1406; DB 1;
Pred. No. 8.2e-97;
4; Mismatches 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACYL-{ACYL-CARRIER PROTEIN] DESATURASE BLOCKED (PARTIAL).
; 7B14529889D39087 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHLOROPLAST
EGPVVPFSWIFDRQVKL
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                                                                                                                                                                                                                                                                                                                                                                                                                        61;
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                             394
396
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STAD_BANA
ID STAD_B
AC 01-STAD_B
AC 01-STAD_B
AC 01-DEC
DT 01-DEC

     Matches
                              Query Match
Best Local
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EMBL; X97325; CAA65990.1; -.
PIR; S23351; S23351.
HSSP; P22337; 1AFR.
InterPro; IPRO05067; FA_desat.
InterPro; IPRO01225; FA_desaturase.
Pfam; PF03405; FA_desaturase_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STAD_BRANA P29108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acyl-[acyl-carrier protein] desaturase, chloroplast precursor
(EC 1.14.99.6) (Stearoyl-ACP desaturase).
                                                                                                                                                                                              PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
Oxidoreductase; Fatty acid biosynthesis; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SUBUNIT: HOMODIMER.
-!- SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PL
NONPHOTOSYNTHETIC TISSUES.
-!- SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             = oleoyl-[acyl-carrier protein] + A + 2 H(2)0.
-i- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE,
-i- PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97260965; PubMed-9107041;
Piffanelli P., Ross J.H., Murphy D.J.;
"Intra- and extracellular lipid composition and associated gene
expression patterns during pollen development in Brassica napus
Plant J. 11:549-562(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core e eurosids II; Brassicales; Brassicaceae; Brassica.
                                                                                                                                                        Transit peptide.
TRANSIT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -:- CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] +
= oleoyl-[acyl-carrier protein] + A + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             stearoyl-acyl carrier protein
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=92212881; PubMed=1557366;
Knutzon D.S., Thompson G.A., Radke
                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=cv.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Modification of Brassica seed oil by antisense modification of Brassica seed oil by antisense gene "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kridel J.C.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -! - FUNCTION: CONVERTS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JNCTION: CONVERTS STEAROYL-ACP
     269;
                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TO UNSATURATED FATTY ACIDS
                                                                                                          398
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     Conservative
                                                                                                                                     ω
5
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                                                                                                                                     398
                                                                                                          45347
                        67.7%;
66.9%;
                                                                                                          MW.
  55;
                                                                                                  CHLOROPLAST (BY SIMILARITY).

ACYL-[ACYL-CARRIER PROTEIN] DESATURASE;

9DD689FCFE41C5F5 CRC64;
                                                      Score
                              Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             desaturase gene.";
89:2624-2628(1992)
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     Mismatches
                No.
                              1396;
No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IN THE SYNTHESIS
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                           5e-96;
                                                                                                                                                                                                            NADP; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Johnson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A
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                                                   Length
  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AH(2) + O(2)
  12;
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Gaps
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MALKLNEQCKK - - NHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP - -

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STAD_SOLGO
ID STAD_S
AC Q41319
AC Q41319
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Q41319;
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15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DUN-2002 (Rel. 41, Last annotation update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acyl-[acyl-carrier protein] desaturase, chloroplast p.
(EC 1.14.99-6) (Stearoyl-ACP desaturase).
Solanum commersonii (Commerson's wild potato).
Solanum commersonii (Commerson's wild potato).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
Spermatophyta; anasterids I; Solanales; Solanaceae; Solar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trucci M., Grillo S., Costa A., Leone A.;
Submitted (APR-1994) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Asteridae; euasterids
NCBI_TaxID=4109;
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                                                       EMBL; X78935; CAA55535.1; HSSP; P22337; 1AFR.
                                                                                                                              modified and this statement is not removed. Usage by entities requires a license agreement (See http://www.or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              = Oleoyl-[acyl-carrier protein] + A + Z H(2)O.

COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.

PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY

ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
                                                                                                                                                                                                                                                                                                                                            SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PI
NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + = oleoyl-[acyl-carrier protein] + A + 2 H(2)0.
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                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation buropean Bioinformatics Institute. There are no restrictions on its
           IPR001225;
                                 IPR005067;
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pr0SITE; pS00574; FATTY_ACID_DESATUR_2; FALSE_NEG.
oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
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elant Mol. Biol. 20:151-155(1992).
-i- FUNCTION: CONVERTS STEAROYL-ACP
-i- FUNCTION: BOND BETWEEN CARBONS
                                                                                                                                                                                                                   Slocombe S.P., Cummins I., Jarvis R.P., Murphy D.J.; "Nucleotide sequence and temporal regulation of a seed-specific Brassica napus cDNA encoding a stearcyl-acyl carrier protein (AV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               174
                                                                                                                                                                                                                                                                          STRAIN=cv. Jet neuf; TISSUE=Embryo; MEDLINE=92385757; PubMed=1515603;
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                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein = oleoyl-[acyl-carrier protein] + A + 2 H(2)O. = (ODACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SAY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OILS.
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.2e-95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     specific,
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                                                                                                           protein] +
                                                                                                                                                DELTA-10 OF THE AC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           394
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                               SATURATED
                                                                                                                                                                                                                                                                                                                                                                                                           a; Tracheophyta;
eudicots; Rosid
                                                                      AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chloroplast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DESATURASE
                                 VEGETABLE
                                                   NADPH.
TED FATTY
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                                                                                                             AH(2)
                                                                                                                                                                                                                                 (ACP)
                                                                                                                                                                                                                                                                                                                                                                                                               Rosidae;
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                                                                                                                 +
                                                                                                                                                    ACYL
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Best Local
                                                                              STAD_SOLTU
P46253;
01-NOV-1995
01-NOV-1995
             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acyl-(acyl-carrier protein) desaturase, chloroplast
(EC 1.14.99.6) (Stearoyl-ACP desaturase).
Solanum tuberosum (Potato).
                                                                                                                                                 SOLTU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL: X63364: CAA44964.1: ..
PIR: S24995; S24995.
HSSP: P22337: 1AFR.
InterPro: IPR005067; FA_desat.
InterPro: IPR001225; FA_desaturase.
Pfam: PF03405; FA_desaturase_2; 1.
PROSITE: PS00574; FATTY_ACID_DESATUR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transit peptide.
TRANSIT 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Some or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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     Eukaryota;
                                                                                                                                                                                                                                                                                                                                          240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 MALKLNFQCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNS---NSMVLDNLKSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: DEVELOPING SEED.

DEVELOPMENTAL STAGE: INDUCED BY 25 DAYS AFTER ANTHESIS (DAA),
PEAKING AT 45 DAA BUT DECREASING CONSIDERABLY THEREAFTER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Chloroplast (
                                                                                                                                                                                                                                                                                          TMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKA
                                                                                                                                                                                                           QEYLCGLTPRIRRLDERAQARAKKGP----KIPFSWIHDREVQL 399
                                                                                                                                                                                                                                           QEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI
                                                                                                                                                                                                                                                                         ANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RERARELPODYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAVWTRAWTAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VHLQVLHSMPPQKIEIFKSMEDRAEQNLLPHLKDVEKSWQPQDFLPDPASDGFEDQVKEL 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVREL 111
                                                                                                                                                                                                                                                                                                                                          GNTARQAKEHGDLKLAQICGTIAADEKRHETAYTKIVEKLLEIDPDGTVVAFADMMRKKI
                                                                                                                                                                                                                                                                                                                                                                                                      NRHGDLLNKYLYLSGRVDMRQTEKTIQYLIGSGMDPRTENNPYLGFIYTSFQERATFVSH
                                                                                                                                                                                                                                                                                                                                                                                                                        NRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MALKFNPLVSQPYKLASSARP-PVSTFRSPKFLCLASSSSPALSSKEVESLKKPFTPPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  265;
 Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399
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399
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65.8%;
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Streptophyta; Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 1386.5; DB Pred. No. 2.3e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHLOROPLAST (BY SIMILARITY)
ACYL-[ACYL-CARRIER PROTEIN]
SEED SPECIFIC.
; 8537254C13D9AF80 CRC64;
                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  66;
                                                                                                                                                                                                                                            394
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                                                precursor
Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                399;
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Best Local S
Matches 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer entities requires a license agreement (See http://www.isb-sib.ch/annou or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Taylor M.A., Smith S.B., Davies H.L., Taylor M.A., Smith S.B., Davies H.L., Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF THE ACYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF03405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; M91238; AAA33839.1; HSSP; P22337; lAFR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4113;
357
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nes 258; Conserv
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SUBCELLULAR LOCATION: CHLORODIAST OF GREEN TISSUE AND PL
NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).

SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  = oleoyl-[acyl-carrier protein] + A + 2 H(2)0.
COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND
PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURAY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACIDS TO UNSATURATED FATTY ACIDS IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATALYTIC ACTIVITY:
                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
                                                                           AHLMYDGSDELLFKHETAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKAQEY
                                                                                                                                                                                                     GDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISHANT
                                                                                                                                                                                                                                                                                                                QVTHSMPPEKIEVFDSLRDWAAQNLLVHLKPVEKCWQPTDFLPDPASEGFDEQVKELRER
                                                                                                                                                                                                                                                                                                                                                                                                          MALKLNFQCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLK---SPP---NL
                             VCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI
                                                                                                                                                      AKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKITMP
                                                                                                                                                                                     GDLLNKYLYLSGRVDMKQIEKTIQYLIGSGMDPRTENNPYLGFVYTSLRKGVTFVSHGNT
                                                                                                                                                                                                                                                                                                                                             QVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELRER 114
                                                                                                                                                                                                                                                                                                                                                                           MALNINGVSLKSHKML----PFPCSSARSERVFMASTIHRPSVEVGSVKKAFTPPREVHV
VCGLAPRIRKLEERAQARAKHAKS----VPFSWIFGKEIKL
                                                            <u>AHLMYDGRDDNLFEHFSAVAQRLGVYTAKDYADILEFHVGRWEVEKLTGLSSEGRRAQDY</u>
                                                                                                                         <u>ARLAKEHGDMKLAQICGSIAADEKRHETAYTKIVEKLLEVDPDGAVLAIGDMMRKNISMP</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PS00574; FA_TTY_ACID_DESATUR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31
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393
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stearoyl-[acyl-carrier protein] + ier protein] + A + 2 H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                          62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1385.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHLOROPLAST (BY SIMILARITY).
ACYL-[ACYL-CARRIER PROTEIN] DESATURASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3FBCC282D57CA7FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                         .7e-95;
les 67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYNTHESIS
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L outstation -
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RESULT
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Acyl-[acyl-carrier protein] desaturase, chloroplast precursor (EC 1.14.99.6) (Stearoyl-ACP desaturase).
Olea europaea (Common olive).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OLEEU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Lamiales; Oleaceae; Olea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 stearoyl-acyl carrier protein desaturase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=cv. Leccino;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=4146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   use by non-profit institutions as long as its content modified and this statement is not removed. Usage by ar entitles requires a license agreement (See http://www.isb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                           Transit peptide.
                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF03405; FA_desaturase_2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                aldoni L., Georgi L., Abbott A.G.;
"Nucleotide sequence of a cDNA clone from Olea europaea encoding
                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                         Oxidoreductase; Fatty acid biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U58141; AAB67840.1; -. HSSP; P22337; 1AFR.
 174
                                 113
                                                                  114
                                                                                                  53
                                                                                                                                54
                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                               H
                                                                                                                                                                                             1 MALKLNFQCKKNHPAAFAKSP-LPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----PN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PL
NONPHOTOSYMPHETIC TISSUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + 0 = 0leoyl-[acyl-carrier protein] + A + 2 H(2)O.

COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plant Gene Register PGR96-052.
FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP
CIS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DE
                                                                                                                                                               MALKL---CFPPH-----KMPSFPDARIRSHRVFMASTIHSPSMEVGKVKKPFTPPREVH 52
                                                 RAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEENR
                                                                                                                             LQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELRE 113
   HGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISHAN
                                VQVTHSLAPEKREIFNSLNNWAQENILVLLKDVDKCWQPSDFLPDSASEGFDEQVMELRK 112
                                                                                                                                                                                                                               266;
                                                                                                                                                                                                                                                                                                390 AA;
                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                390
44596 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Mesocarp;
L., Abbott A.G.;
                                                                                                                                                                                                                                                67.2%;
66.3%;
                                                                                                                                                                                                                                   55;
                                                                                                                                                                                                                                                Score 1385; DB 1
Pred. No. 2.9e-95
                                                                                                                                                                                                                                                                                                CHLOROPLAST (BY SIMILARITY)
ACYL-[ACYL-CARRIER PROTEIN]
; 39090E432B7AC2E3 CRC64;
                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              390
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                                                                                                                                                                                                                                                                                                                                                                NADP; Chloroplast;
                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DELTA-10
                                                                                                                                                                                                                                                                                                                 PROTEIN] DESATURASE
                                                                                                                                                                                                                                                                 Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY INTRODUCTION OF ELTA-10 OF THE ACYL
                                                                                                                                                                                                                                    Indels
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STAD_GOSHI STANDARD; PRT; 397 AA. 042770; 042770; 05-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 47, Last annotation update) 15-JUN-2002 (Rel. 41, Last annotation update) Acyl-lacyl-carrier protein) desaturase, chloroplast (EC 1.14.99.6) (Stearcyl-ACP desaturase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; viridiplantae; Streptophyta; Embry
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Malvales; Malvaceae; Gossypium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOSHI
                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entities requires a license agreement (See lor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gossypium hirsutum (Upland cotton)
                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3635;
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                                                                                                                                                             EMBL; X95988; CAA65232.1; -. HSSP; P22337; 1AFR.
                                                                                                                                                                                                                                                                                                               -
                                       SEQUENCE
                                                                                                                     Pfam; PF03405;
                                                                  TRANSIT
                                                                              Transit peptide.
                                                                                            Oxidoreductase; Fatty acid
                                                                                                         PROSITE;
                                                                                                                                    InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase
                                                                                                                                                                                                                                                                                                                                                                            CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(2) + (= oleoyl-[acyl-carrier protein] + A + 2 H(2)O.

COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE
                                                                                                                                                                                                                                                                                                              SUBUNIT: HOMODIMER (BY SIMILARITY)
SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS
NONPHOTOSYMPHETIC TISSUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PAHLMYDGSDELLEKHFTAVAGRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKAQE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cv. Deltapine 16;
Singh S., Sharp
                                                                                  03405; FA_desaturase_2; 1.
03405; FA_desaturase_2; 1.
ps00574; FATTY_ACID_DESATUR_2; 1.
ps00574; Fatty acid biosynthesis; NADP; Chloroplast;
                                         34
397 i
                                         ΑĄ,
                                                        397
                                         45233 MW;
                                                                    \frac{3}{3}
  66.7%;
67.7%;
                                         ACYL-[ACYL-CARRIER PROTEIN] DESATURASE
5FAA220238B2C37A CRC64;
                                                                    CHLOROPLAST (BY SIMILARITY)
  Score 1375.5;
Pred. No. 1.5e-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          397
                                                                                                                                                                                                                    moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                 There are no restrictions ng as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Embryophyta;
edons; core e
                 DB
                 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY INTRODUCTION OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    eudicots;
                 Length 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tracheophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                         AH(2) + O(2)
                                                                                                                                                                                                                                       for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rosidae;
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                                                                                                                                                                                                                                       n no way commercial
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Matches

272;

Conservative

41;

Mismatches

76;

Indels

13;

6;

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ID STAD_D
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DT 15-DI
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15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
16-JUN-2002 (Rel. 41, Last annotations update)
Acyl-[acyl-carrier protein] desaturase, chloroplast p
(EC 1.14.99.6) (Stearoyl-ACP desaturase).
Elaeis quineensis var. tenera (Oil palm).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Arecaceae;
Cocceae; Elaeidinae; Elaeis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Nucleotide sequence of a cDNA clone encoding stearoyl-acyl-carrier-protein from Elaeis quineensis var tenera.";
(In) Plant Gene Register DGR96-110.
-i- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION OF CIS_DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL-CIS_DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE ACYL
                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                   - oleoyl-[acyl-carrier protein] + A + 2 H(2)U.
- oleoyl-[acyl-carrier protein] + A + 2 H(2)U.
- COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH.
- COFACTOR: FERREDOXIN, FERREDOXIN CONVERSION OF SATURATED FATTY
PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY
ACTOR IN THE SYNTHESIS OF VEGETABLE
                                                                                                                                                                                                                                                 SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PL
NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + - oleoyl-[acyl-carrier protein] + A + 2 H(2)0.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     STAD_SIMCH STANDARD; PRT; 398 AA. (Q01753; Q01753; Q01753; Q1764; Q1753; Q1764; Q1763; Q1764; Q1763; Q1764; Q1766; Q1766;
                                                                                                        SEQUENCE FROM N.A., Knauf V.C.;
Sato A., Becker C.K., Knauf V.C.;
Nucleotide sequence of a complementary DNA clone encoding acyl carrier protein desaturase from Simmondsia chinensis.*
Plant Physiol. 99:362-363(1992).
-I- FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTROIOTE NORTHLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 O
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryop
Spermatophyta; Magnoliophyta; eudicotyledons; c
Caryophyllidae; Caryophyllales; Simmondsiaceae;
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Pfam; PF03405; FA_desaturase_2; 1.

PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.

Oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
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HSSP; P22337; 1AFR.
                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
Sato A., Becker C.K.,
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CHAINTIC ACTIVITY: Stearoyl-[acyl-carrier protein] + AH(
- oleoyl-(acyl-carrier protein] + A + 2 H(2)0.

COFACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NAI

PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED
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No. 2.2e-94;
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2096.56;
37, Created)
T 15-DEC-1998 (Rel. 37, Last sequence update)
T 15-DEC-1998 (Rel. 41, Last annotation update)
T 15-UN-2002 (Rel. 41, Last annotation update)
E Acyl-[acyl-carrier protein] desaturase, chloroplast prec (EC 1.14.99.6) (Stearoyl-ACP desaturase)
E (EC 1.14.99.6) (Stearoyl-ACP desaturase)
DE (EC 1.14.99.6) (Stearoyl-ACP desaturase)
S Helianthus annuus (Common sunflower)
S Helianthus annuus (Common sunflower)
C Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trace (Common sunflower)
C Spermatophyta; Magnoliophyta; eudicotyledons; Core eudico
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Interpro: IPR001225; FA_desaturase.
Pfam; PF03405; FA_desaturase_2; 1.
PROSITE: PS00574; FATTY_ACID_DESATUR_2;
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by non-profit institutions as long as its content
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Coughlan S.J., Hastings C.E., Winfrey R.J.;
Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
-i-FUNCTION: CONVERTS STEAROYL-ACP TO OLEOYL-ACP BY INTRODUCTION
CITS DOUBLE BOND BETWEEN CARBONS DELTA-9 AND DELTA-10 OF THE AC
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TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Heliantheae; Helianthus NCBI_TaxID=4232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            prosite; ps00574; FATTY_ACID_DESATUR_2; 1.
oxidoreductase; Fatty acid biosynthesis; NADP; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR005067; FA_desat.
InterPro; IPR001225; FA_desaturase.
InterPro; IPR001225; FA_desaturase.2; 1.
Pfam; PF03405; FA_desaturase.2; 1.
PROSITE; PS00574; FATTY_ACID_DESATUR_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; U70374; AAB09571.1; -. HSSP; P22337; 1AFR.
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  357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MALKLN---FOCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARALYTIC ACTIVITY: Stearoy1-[acy1-carrier protein] + AH(2) + (2) - oleoy1-[acy1-carrier protein] + A + 2 H(2)O. - oleoy1-[acy1-carrier protein] + A + 2 H(2)O. - COPACTOR: FERREDOXIN, FERREDOXIN NADPH REDUCTASE, AND NADPH. PATHWAY: CATALYZES THE PRINCIPAL CONVERSION OF SATURATED FATTY ACIDS TO UNSATURATED FATTY ACIDS IN THE SYNTHESIS OF VEGETABLE OILS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SUBUNIT: HOMODIMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CHLOROPLAST OF GREEN TISSUE AND PLASTIDS NONPHOTOSYNTHETIC TISSUES (BY SIMILARITY).
SIMILARITY: BELONGS TO THE FATTY ACID DESATURASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                     MAIRINTATFQSDLYRSFAFPQ-PKP---LRSPKFAMASTIGSATTKVESTKKPFTPPRE
                                                                        RERAKBIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEE
                                                                                                                                                                                                                                                                                                                                                                                   266;
ANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKI
                                                                                                                                                                                                                            {\tt NRHGDLLHQYLYLSGRVDMRQIQKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFISH}
                                                                                                                                                                                                                                                  NRHGDLLNKYLYLSGRYDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISH
                                                                                                                                                                                                                                                                                                           RARAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGATLLLGLVWTRAWTAEE
                                    QEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide.
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396 AA;
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45078 MW;
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Pred. No. 8.1e-93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACYL-[ACYL-CARRIER PROTEIN] DESATURASE, 97E455A116791B81 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHLOROPLAST (BY SIMILARITY)
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Search completed: December 1, 2002, 21:20:34 Job time : 16 secs

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Result
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Perfect score:
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence:
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                                                                                                                                                                                                                                                                                                          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
  1441.5
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2062
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Listing first 45 summaries
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/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980_DAT:*
/SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1990_DAT:*
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/SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981.DAT:*
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AAR76578
AAW44350
AAR14189
AAB48199
AAR20011
AAW37939
AARW37939
AAR14188
AAR22048
AAR24048
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                                                                                                                                                                                                             Description
                Carthamus tinctori
Sequence encoding
                                                      Amino acid sequenc
C. tinctorius delt
                                                                                             Mature castor enzy
Soybean seed stear
                                                                                                                                                      Coriander omega-12
Ricinus communis d
                                                                                                                                 R. communis delta9
tinctor
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	AAG8092	22	11/	•	1215
ᄑ	ABB92	23	396	59.2	1220
Herbicidally	AΒ	23	401	•	1223.5
그 :	ABB9	23	411		24
Arabidops	AAG4	21	321	•	28
	AAG29	21	321	•	28
abic	AAG2	21	321	•	28
Delta 9-fat	AAR96	17	390	•	31
Arabidopsis	AAG18	21	395	•	S
Herbicidally	ABB93	23	394	•	$\frac{\omega}{2}$
Arabidops	AAG18	21	393	•	ω
Arabidops	AAG18	21	391	•	3
Corn delta-	AAY32	21	392	•	1324
Arabidopsi	AAG45	21	332	٠	(L)
Arabidops	AAG29	. 21	332	•	1335.5
Arabidopsis	AAG22	21	332	•	w
Arabidops	AAG16	21	439	•	1355
Arabidops	AAG16	21	396	•	1355
Arabidops	AAG16	21	394		1355
Herbicidally	ABB92	23	396		1356
Corn delt	AAY32	21	392	•	1364
Amino acid	AAY68	21	363	•	1372
Cotton stea	AAE13	22	396	٠	1377
A. thaliana	ABB07	23	401		38
Herbicidally	ABB92	23	401	•	38
Arabidopsis	AAG29	21	401	•	38
Delta-9-de	AAR47	15	399	•	1383.5
Amino aci	AAY68	21	393	•	38
Zea mays	AAY09	18	393		38
Brassica	AAW4	19	398		1396
Rapeseed	AAW14	18	398	67.7	1396
B. campes	AAR14	12	398		1396
Rapeseed	AAW14	18	401	•	40
Stearoy1-	AAR82024	16	76£	•	1404.5

ALIGNMENTS

RESULT 1 AAR76578 YXX PDX XX X X Cahoon EB, 07-AUG-1992; 07-AUG-1992; 04-JUL-1995 Protein Coriandrum Coriander; omega-12 desaturase; petroselenic acid; transgenic plant; crop improvement; tobacco. Coriander omega-12 desaturase 05-DEC-1995 (first entry) AAR76578; AAR76578 standard; Protein; 385 AA US5430134-A Key (UNMS) UNIV MICHIGAN STATE Peptide sativum. Ohlrogge JB, Shanklin J, 92US-0926788 92US-0926788 /label= Plastid_transis_peptide
36..385 Location/Qualifiers /label= Mat_protein Somerville CR;

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RESULT 2
AAW4 4350
ID AAW4
XX
AC AAW4
XX
DT 28-j
DE Ric
XX
Ric
XX
Ric
XX
Ric
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Ri
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OS Ri
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Best Local :
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N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A CDNA library prepd. from developing seeds of coriander was screened with a probe based on a partial cDNA clone (AAQ92889) of omega-12 desaturase to isolate full-length clone EC201 (AAQ92889). Expression of this cDNA in transgenic tobacco callus resulted in prodn. of petroselenic acid (18:1 omega 12) and omega-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Columns 18; 25pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hexadecenoic acid
                                                                                                                                                                                                                                             AAW44350 standard;
  16-SEP-1991;
16-MAR-1990;
                                                             03-MAR-1998
                                                                                                                                                                                               28-MAY-1998
                                       06-JUN-1995;
                                                                                                                                                                                                                                                                                                       343
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         omega-12 desaturase from coriander - and DNA encoding it, making transgenic plants able to synthesise petroselenic \dot{a}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1995-253884/33.
DB; AAQ92889.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MALKLN----FQCKKNHPAAFAKSPLPVTRVSSP-----RVFMASTVNSNSMVLDNLK 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAMKLNALMTLQCPKRN-----MFTRIAPPQAGRVRSKVSMASTLHASPLVFDKLK
                                                                                                                                                                                                                                                                                                                                                    SPPNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVR 109
                                                                                                                                                                                                                                                                                                                                                                                                    SHANTAKLAQHYGDKNLAQVCGNIASDEKRHATAYTKIVEKLAEIDPDTTVIAFSDMMRK
                                                                                                                                                                                                                                                                                                                                                                                                               SHANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EENRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFI
                                                                                                                                                                                                                                                                                                       KAQEYVCSLAAKIRRVEEKVQGKE--KKAVLPVAFSWIFNRQIII 385
                                                                                                                                                                                                                                                                                                                    KAQEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                   EENRHGDLLNKYLYLSGRVDMRMIEKTIQYLIGSGMDTKTENCPYMGFIYTSFQERATFI
                                                                                                                                    acid saturation.
                                                                                                                                                                        communis
                                                                                                                                                communis; castor bean;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           385 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ----RPEVDELFNSLEGWARDNILVHLKSVENSWQPQDYLPDPTSDAFEDQVK 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                               (first entry)
   91US-0762762
90US-0494106
                                        95US-0471791.
                                                                                                                                                                        desaturase
                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75.0%;
73.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1545.5; DB 1
Pred. No. 7.3e-140;
42; Mismatches 36;
                                                                                                                                                                                                                                                396
                                                                                                                                                                        from clone
                                                                                                                                                  delta-9
                                                                                                                                                                        pcgN3230
                                                                                                                                                  desaturase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                  394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful
acid.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                289
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      222
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AAR14189
ID AAR1
XX
AC AAR1
XX
DT 11-D
XX
DE R. C

AAR14189

standard;

Protein;

396

A

R. communis delta9 11-DEC-1991

desaturase

from

(first entry)

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Best Loc
Matches
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14-NOV-1990;
14-MAR-1991;
06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents a Ricinus communis desaturase from clone pCGN3230. The present invention describes a recombinant DNA construct comprising a DNA sequence encoding a plant Delta-9 desaturase protein. The present invention also provides a method of modifying fatty acid composition in a host plant cell from a given fatty acid saturation to a different fatty acid saturation, comprising growing a host plant cell containing a recombinant DNA sequence which encodes a plant desaturase under the control of regulatory elements functional in the plant cell during lipid accumulation. Also, oilseeds having a modified level of fatty acid saturation and oils produced from such oilseeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding plant delta-9 desaturase protein - having sequence of Carthamus tinctorius desaturase, useful for producing oil-seeds with modified levels of fatty acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CALJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Knauf VC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 7; Column 59-60; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; AAV15252
                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                              234
                                                                                                                                     179
                                                                                                                                                           174
                                                                                                                                                                                119
                                                                                                                                                                                                                                                                                                                             Local
                                                                                          239
  359
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                                                                                                                                                                                                                                                                         _
                                                                                                                                                                                                                                                                                                                                         Match
                                                                                                                                                                                                                                                                                           1 MALKLN-FOCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----PN 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1998-178544/16.
                                                                                                                                                                                                                          RAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEENR 173
                                                                                                                                                                                                                                                                      RAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAEENR
                                                                                                                                                                                                                                                                                                                    al Similarity
286; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) CALGENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thompson
                                                                                                                                                                                                                                                                                                                                                                 396 AA;
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            90US-0567373.
90US-0615784.
91WO-US01746.
95US-0471791.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INC.
                                                                                                                                                                                                                                                                                                                               72.3%;
71.1%;
                                                                                                                                                                                                                                                                                                                    ; Score 1490; DB 19;
; Pred. No. 1.7e-134;
50; Mismatches 52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 n - having amino useful for, e.g.
                           394
                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               saturation
                                                                                                                                                                                                                                                                                                                        14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid
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Best Local
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16-MAR-1990;
13-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              increased percentage of unsatd. fatty acids may be provided, using anti-sense technology, the amt. of desaturase can be decreased, resulting in a higher percentage of fatty acids. Using the desaturase gene and derivs. in cells and plants, desirable traits such as chill tolerance may be introduced and environmentally safe herbicide prods. may be provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modification of fatty acid in a plant host cell to a different percentage of fatty acid sath, is possible by growing a host plant cell having integrated into its genome a recombinant DNA sequence encoding this protein, under the control of regulatory elements functional in the plant cell during lipid accumulation, under conditions which will promote the activity of the regulatory elements. By increasing the amt. of desaturase available in plant cells, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 3B; 128pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Thompson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA encoding a plant desaturase - used for modifying the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19-SEP-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ricinus communis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desaturase; fatty acid; saturation; chill tolerance; lipid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CALG-) CALGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  herbicide
                                                                                                                          179
 299
                                294
                                                              239
                                                                                          234
                                                                                                                                                         174
                                                                                                                                                                                       119
                                                                                                                                                                                                                    114
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                                                                                                                                                                                                                                                                                54
                                                                                                                                                                                                                                                                                                                                          1 MALKLN-FQCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----PN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      also AAQ13963-69.
                                                                             TAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKITM
                                                                                                                                                                                                                                                                LQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELRE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1991-295627/40
PAHLMYDGRDDNLFDHFSAVAQRLGVYTAKDYADILEFLVGRWKVDKLTGLSAEGQKAQD
                             PAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKAQE
                                                             TARQAKEHGDIKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKISM
                                                                                                                                                     HGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISHAN
                                                                                                                                                                                    RAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVGDETGASPTSWAIWTRAWTAEENR 178
                                                                                                                                                                                                                   RAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEENR 173
                                                                                                                                                                                                                                                 VQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEKCWQPQDFLPDPASDGFDEQVRELRE 118
                                                                                                                                                                                                                                                                                                             MALKLNPFLSQTQKLPSFALPPMASTR--SPKFYMASTLKSGSKEVENVKKPFMPPREVH 58
                                                                                                                        HGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFISHGN
                                                                                                                                                                                                                                                                                                                                                                            284;
                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAQ13964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 compsn. of plant cells and plant seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                       396 AA;
                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Knauf V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90US-0494106
90US-0567373
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         91WO-U001746
                                                                                                                                                                                                                                                                                                                                                                                       71.8%;
                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                                                                                                         Score 1480;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         DB 12;
L.5e-133;
                                                                                                                                                                                                                                                                                                                                                                                                       Length 396;
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                                                                                                                                                                                                                                                                                                                                                                         14;
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 358
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RESULT 4
AAB48199
ID AAB4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           XXX DE
                                                                 The invention relates to a new mutant castor Delta9-18:0-acyl carrier protein (ACP) desaturase that has one or more amino acid substitutions selected from: (a) Ala for Met at residue 114; (b) Arg for Thr at residue 117; (c) Gly for Leu at residue 118; (d) Val for Pro at regidue 179; (e) Val for Thr at residue 181; (f) Leu for Gly at residue 188; and (g) Phe for Thr at residue 181. The mutant castor Delta9-18:0-ACP desaturase is useful in producing commercially useful products, such as vegetable oils rich in monounsaturated fatty acids. Such vegetable oils are important in human nutrition and can be used as renewable sources of industrial chemicals. A method for specifically altering a function of a protein through directed mutagenesis is also provided. The method can be used altering enzymatic functions, binding functions or structural functions of a protein the desaturation of a protein call the castor desaturation.
                                          of the castor desaturase enzyme. The method is also useful for manipulating the physical properties and commercial uses of conventional
                                                                                                                                                                                                                                                                                         New mutant castor Delta9-18:0-Acyl Carrier Protein desaturase, useful in producing commercially valuable products, e.g. vegetable oils useful in human nutrition or as industrial chemicals \cdot
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note=
Misc-difference 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Misc-difference 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
Misc-difference 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ricinus communis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Castor; delta9-18:0-acyl carrier protein desaturase; ACP; enzyme;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    02-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAB48199;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB48199 standard;
                            plant oils.
                                                                                                                                                                                                                                                                                                                                                                                               Shanklin
                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-JUN-2000; 2000WO-US15741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-DEC-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200075170-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mature castor enzyme
                                                                                                                                                                                                                                                              Examples; Fig 1; 53pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                           (BROO-) BROOKHAVEN SCI ASSOC LLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vegetable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   359
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                                                                                                                                                                                                                                                                                                                                                                  2001-091202/10
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                                                                                                                                                                                                                                                                                                                                                    AAC84531
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           oil; fatty acid; nutrition; plant oil; mutant.
                            The present sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                        99US-0328550
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188
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "can be substituted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    be
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     substituted
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                            represents the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ala"
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                               mature
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                               castor
                              enzyme
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DB 22;

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RESULT 5
AAR20011
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Best Local :
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                                                                                                                                                                                                                                         Glycine max strain Cultivar Wye
                                                                                                                                                                                                                                                                           Soybean seed
                                                                                                                                                                                                                                                                                             31-MAR-1992
                                                                                                                                                                                                                                                                                                                               AAR20011 standard; Protein; 391
                                                          WPI; 1992-007469/01.
N-PSDB; AAQ20187.
                                                                                                                                                                                                                                                         soya bean; plant oil; stearic acid
                         DNA encoding soybean stearoyl-ACP desaturase enzyme and precursor - and chimeric genes, for plant transformation and control of levels of satd. and unsaturated fatty acids in edible oils
                                                                                                                                                                                              Protein
          Disclosure;
                                                                                       Hitz WD,
                                                                                                                          25-MAY-1990;
                                                                                                                                           16-MAY-1991;
                                                                                                                                                           12-DEC-1991
                                                                                                                                                                             WO9118985-A
                                                                                                                                                                                                               Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181
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                                                                                                       (DUPO)
                                                                                                                                                                                                                                                                                                                                                                                                                              329
                                                                                                                                                                                                                                                                                                                                                                                                                                               241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 73.8 nes 271; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ľ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VRDETGASPTSWAIWTRAWTAEENRHGDLLNKYLYLSGRVDMRQIEKTIQYLIGSGMDPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IKDETGAEPSAWAMWTRAWTAEENRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASTLKSGSKEVENLKKPFMPPREVHVQVTHSMPPQKIEIFKSLDNWAEENILVHLKPVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASTVNSNSMYLDNLKSP-----PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEK 88
                                                                                                                                                                                                                                                                                                                                                                                    FNRELKI 394
                                                                                                                                                                                                                                                                                                                                                                                                           EKLFEIDPDGTVLAFADMMRKKISMPAHLMYDGRDDNLFDHFSAVAQRLGVYTAKDYADI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SENSPYLGFIYTSFQERATFISHANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIV 268
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EKLAEIDPDTTVIAFADMMRKKITMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDI
                                                                                                                                                                                                                                                                                                                                                                           FDRQVKL 363
                                                                                                        DU PONT DE
                                                                                       Yadav N;
         Page 54;
                                                                                                                                                                                                                                                                           stearoyl-ACP desaturase
                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                          90US-0529049.
                                                                                                                                            91WO-US03288
                                                                                                                                                                                               /label= transit 33..391
                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                          NEMOURS CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    69.9%;
73.8%;
          70pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            45; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 1441.5; DB 2
Pred. No. 6.8e-130;
                                                                                                                                                                                                                                                                                                                                 ΑA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 363;
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                                                                                                                                                                                                                                                                                                                              RESULT 6
AAW37939
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Best Local Sin
Matches 278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Levels of saturated and unsaturated fatty acids can be controlled in plants, e.g. oilseed rape, sunflower, soybean, peanut, etc., transformed with nucleic acid sequences coding for the expression of this enzyme.
         07-JUN-1995;
19-MAY-1991;
11-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 See also AAQ20188-Q20190
                                                                                                                               Protein
                                                                                                                                                              Key
                                                                                                                                                                                    Glycine max.
                                                                                                                                                                                                       Soybean stearoyl ACP-desaturase; chimeric gene; antisense; transformation; saturated fatty acid; unsaturated fatty acid; soybean oil; inhibition; polyunsaturate; monosaturate.
                                                                                                                                                                                                                                                                                                                     AAW37939 standard; Protein;
                                                     07-JUN-1995;
                                                                           02-JUN-1998
                                                                                                US5760206-A.
                                                                                                                                                                                                                                                    Amino acid sequence
                                                                                                                                                                                                                                                                          21-AUG-1998
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                                                                                                                                                    Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WTAEENRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QVKELRERAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTSWAIWTRA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TPPREVHVQVTHSMPPQKIEIFKSLEDWADQNILTHLKPVEKCWQPQDFLPDPSSDGFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ----PNLQVTHSMPPQKLETFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MALRLN------PIPTQTFSLPQMPSLRSPRFRMASTLRSGSKEVENIKKPF
                                                                                                                                                                                                                                                                                                                                                                                                                  MRKKITMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSD 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                             QVRELRERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WTAEENRHGDLLNKYLYLSGRVDMKQIEKTIQYLIGSGMDPRTENSPYLGFIYTSFQERA
                                                                                                                                                                                                                                                                                                                                                                          EGRKAQEYVCGLPPRIRRLEERAQARGKESST----LKFSWIHDREV
                                                                                                                                                                                                                                                                                                                                                                                     EGRKAQEYVCELGPKIRRVEEKVQGKEKKKAEHPVSFSWIFNREL 392
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                                                                                                                                                                                                                                                                          (first entry)
         95US-0474587.
91WO-US03288.
92US-0995657.
                                                     95US-0474587
                                                                                                                                                    Location/Qualifiers
                                                                                                                               /note= "transit peptide"
33..391
                                                                                                                       /note=
                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               69.7%;
                                                                                                                                                                                                                                                      the soybean
                                                                                                                      "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; Score 1436.5; DB 10; pred. No. 2.3e-129; 44; Mismatches 53;
                                                                                                                                                                                                                                                                                                                       391
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                                                                                                                                                                                                                                                      seed
                                                                                                                                                                                                                                                      stearoyl-ACP desaturase
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RESULT 7
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XX AAR1
AC AAR1
XX II-C
DT 11-C
XX DES C. t
XX Desa
KW hert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             chimeric genes which are used in (antisense orientation) to transform plant cells. The nucleic acids are useful for controlling the levels of (un)saturated fatty acids in soybean oll. In transformed cells (seeds), the chimeric genes transcribe the antisense RNA to the complementary mRNA for the enzyme. This results in inhibition of expression of the endogenous enzyme and reduction in desaturation of seed oil. This results in seed oil which is low in saturates and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding soybean seed stearoyl-ACP desaturase enzyme are useful for the anti-sense inhibition of the enzyme in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transformed
                herbicide
                                 Desaturase; fatty acid; saturation; chill tolerance; lipid;
                                                                                                                               AAR14188
                                                                                                                                                              AAR14188 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                 tinctorius delta9 desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MALKLNFQCKKNHPAAFAKSPLPVTRVS-----SPRVFMASTVNSNSMVLDNLKSP- 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            is the amino acid sequence of soybean stearoyl ACP-desaturase in the method of the invention, which involves the creation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1998-332247/29
                                                                                                                                                                                                                                                                                                                             MRKKITMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSD 346
                                                                                                                                                                                                                                                                                                                                                                         TFISHGNTARLAKEHGDIKLAQICGMIASDEKRHETAYTKIVEKLFEVDPDGTVMAFADM
                                                                                                                                                                                                                                                                                                                                                                                                       TFISHANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QVKELRERAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTSWAIWTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QVRELRERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TPPREVHVQVTHSMPPQKIEIFKSLEDWADQNILTHLKPVEKCWQPQDFLPDPSSDGFEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALRLN------PIPTQTFSLPQMPSLRSPRFRMASTLRSGSKEVENIKKPF
                                                                                                                                                                                                                                                                           EGRKAQEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNREL 392
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                                                                                               entry)
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68.5%;
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Pred. No. 2.3e-129;
                                                               from pCGN274
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cell having integrated into its genome a recombinant DNA sequence encoding this protein, under the control of regulatory elements functional in the plant cell during lipid accumulation, under conditions which will promote the activity of the regulatory elements. By increasing the amt. of desaturase available in plant cells, an increased percentage of unsatd fatty acids may be provided, using anti-sense technology, the amt. of desaturase can be decreased, resulting in a higher percentage of fatty acids. Using the desaturase gene and derivs. in cells and plants, desirable traits such as chill tolerance may be introduced and environmentally safe herbicide prods. may be provided.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-NOV-1990;
16-MAR-1990;
13-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA encoding a plant desaturase - used for modify fatty acid compsn. of plant cells and plant seeds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thompson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               W09113972-A
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2; 128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-MAR-1991;
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                                                                                                                                                                                                                                                                                                                                         1 MALKL---NFQCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----
                TMPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKA
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                                               NRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISH
                                                                                                                                                                             RARAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTPWAVWTRAWTAEE
                                                                                                                                                                                              RERAKEIPDDYFVVLYGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEE 171
                                                                                                                                                                                                                                             VHVQVTHSMPPQKIEIFKSIEGWAEQNILVHLKPVEKCWQAQDFLPDPASEGFDEQVKEL
                                                                                                                                                                                                                                                                           PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVREL
                                                                                                                                                                                                                                                                                                           MALRITPVTLQSERYRSFSFPKK----ANLRSPKFAMASTLGSSTPKVDNAKKPFQPPRE
                                                                             ANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKI
{\tt NRHGDLLHTYLYLSGRVDMRQIQKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFVSH}
                                                                                                                                                                                                                                                                                                                                                                         271;
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90US-0567373
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34..396
/label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                       68.2%;
67.1%;
                                                                                                                                                                                                                                                                                                                                                                         54;
                                                                                                                                                                                                                                                                                                                                                                        Score 1406; DB 12;
Pred. No. 2e-126;
4; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    used for modifying the
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satd

Length Indels

18;

Gaps

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56 51

291

236

177

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AAR22048
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Db
                                                                                                                                                                              Matches
                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                 The protein sequence was deduced from the desaturase gene isolate from Carthamus tinctorius as the clone pCGN2754. The clone can bused to construct acyl carrier protein expression cassettes in a binary vector for plant transformation. This allows integration of nucleic acids encoding a desaturase sequence and a synthase sequence into the genome of a host cell. A plant desaturase includes any enzyme capable of catalysing the insertion of a first double bond into a fatty acid-ACP moiety especially between C9-C1 See also AAR22046-53.
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 8; 157pp; English.
                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Knauf VC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-JUN-1991;
15-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09203564-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carthamus tinctorius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Safflower;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carthamus tinctorius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JUL-1992
      172
                             117
                                                                                                                                                                                                                                                                                                                                                                                                              New plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-AUG-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lipids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR22048;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR22048
                                                     112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CALG-) CALGENE
                                                                               57
                                                                                                      52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     297
                                                                                                                               μ
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NRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISH
                                                                          VHVQVTHSMPPQKIEIFKSIEGWAEQNILVHLKPVEKCWQAQDFLPDPASEGFDEQVKEL
                                                                                     RERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEE
                                                                                                                                                 MALKL---NFQCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----
                         RARAKEIPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTPWAVWTRAWTAEE
                                                                                                                          MALRITPVTLQSERYRSFSFPKK----ANLRSPKFAMASTLGSSTPKVDNAKKPFQPPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                   1992-096907/12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QDYVCGLPPRIRRLEERAQGRAK----EGPVVPFSWIFDRQVKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QEYVCELGPKIRRVEEKVQGKEKKKKAEHP-VSFSWIFNRELKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMPAHLMYDGRDDNLFEHFSAVAORLGVYTAKDYADILEFLVGRWKVADLTGLSGEGRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAQ22616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                             beta-keto:acyl synthase protein - obtd. from useful e.g. for modifying fatty acid compsn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thompson
                                                                                                                                                                                                                            396 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fatty acid synthesis; seed; acyl carrier protein;
                                                                                                                                                                           68.2%; ilarity 67.1%; Conservative 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91US-0721761.
90US-0568493.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91WO-U005801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                desaturase
                                                                                                                                                                         ; Score 1406; DB 13;
; Pred. No. 2e-126;
54; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AΑ
                                                                                                                                                                                                                                                            especially between C9-C10
                                                                                                                                                                           Indels
                                                                                                                                                                                                 Length
                                                                                                                                                                                                                                                                                                                                                                                                           Ricinus
                                                                                                                                                                                                 396;
                                                                                                                                                                                                                                                                                                                                    isolated
ne can be
                                                                                                                                                                           18;
                                                                                                                                                                                                                                                                      first
                                                                                                                                                                        Gaps
                                                171
                                                                        116
  231
                                                                                                                                                 51
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DЪ Qy

1 MALKL --- NFQCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----MALRITPVTLQSERYRSFSFPKK----ANLRSPKFAMASTLGSSTPKVDNAKKPFQPPRE

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RESULT 9
AAR54033
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Db
 Query Match
Best Local S
Matches 271
                                                                          constructs containing anti-sense synthase sequences. The constructs allow the generation of plants bearing seeds which have enhanced of yields and/or altered compositions of oils. The production of common plant unsaturated fatty acids is catalysed by a desaturase. Oleic, linoleic and alpha-linoleic acids found in storage triglycerides are produced from the desaturation of stearoyl-ACP to
                                                                                                                                             Higher plants appear to share a common metabolic pathway for the synthesis of fatty acids. Genes encoding synthase proteins may be used in nucleic acid constructs to modulate the amount of synthase activity in a host cell. Nucleic acid constructs may also be designed to decrease the expression of a synthase protein, i.e.,
                                               Sequence
                                                                     form oleoyl-ACP.
                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                      DNA constructs encoding beta-keto:acyl-\LambdaCP synthase - usef modify the oil content of seeds, e.g. for dietary purposes
                                                                                                                                                                                                                                                                           N-PSDB; AAQ64003
                                                                                                                                                                                                                                                                                      WPI; 1994-167378/20
                                                                                                                                                                                                                                                                                                                                                       02-NOV-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 C. tinctorius
                                                                                                                                                                                                                                                                                                             Knauf VC,
                                                                                                                                                                                                                                                                                                                                                                             02-NOV-1993;
                                                                                                                                                                                                                                                                                                                                                                                                    11-MAY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthase; plants;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-DEC-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR54033 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR54033;
                                                                                                                                                                                                                                                                                                                                  (CALJ ) CALGENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     292
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEYVCELGPKIRRVEEKVQGKEKKKKAEHP-VSFSWIFNRELKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QDYVCGLPPRIRRLEERAQGRAK----EGPVVPFSWIFDRQVKL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NRHGDLLHTYLYLSGRVDMRQIQKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFVSH
 Similarity 67.71; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       encoding desaturase
                                                                                                                                                                                                                                                                                                          Thompson
                                               396
                                                                                                                                                                                                                  Figure 10; 85pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                               ΑA;
                                                                                                                                                                                                                                                                                                                                                        92US-0971182
                                                                                                                                                                                                                                                                                                                                                                             93WO-US10526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 oil;
              68
67
            .1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            396
 Score 1406; DB 15;
Pred. No. 2e-126; '
4; Mismatches 61;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fatty acids;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ĄΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expression;
                     Length
 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       394
                                                                                                                                    The constructs
                                                                                                                                                                                                                                                    useful
                      396;
 18;
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Gaps
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RESULT 10

AAW444349

ID AAW44

XX AAW4

XX 28-MA

XX Carth

XX Carth

XX Carth

XX FT Pepti

FT Prote

FT Prote

FT Prote

FT Prote

XX 03-MA

XX 03-MA

XX 06-JU

PR 11-SE

PR 11-SE

PR 11-AU

PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Вþ
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                                                                                                                                                                                                                                                                                                                                               16-SEP-1991;
16-MAR-1990;
13-AUG-1990;
14-NOV-1990;
14-MAR-1991;
06-JUN-1995;
                                                                                                               DNA encoding plant delta-9 desaturase protein - having amino acid sequence of Carthamus tinctorius desaturase, useful for, e.g.
                                                                                                                                                                                     WPI; 1998-178544/16.
N-PSDB; AAV15250.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carthamus tinctorius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Carthamus tinctorius;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carthamus
                                          Claim 5; Column 53-56; 87pp; English
                                                                                                                                                                                                                                                          Knauf VC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAW44349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW44349 standard;
                                                                                                                                                                                                                                                                                                    (CALJ ) CALGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US5723595-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAY-1998
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  present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TMPAHLMYDGSDELLFKHFTAVAQRVXYYSALDYCDILEFLYDKWNVERLTGLSDEGRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMPAHLMYDGRDDNLFEHFSAVAQRLGVYTAKDYADILEFLVGRWKVADLTGLSGEGRKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GNTARHAKDHGDVKLAQICGTIASDEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKI 291
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRHGDLLHTYLYLSGRVDMRQIQKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFVSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VHVQVTHSMPPQKIEIFKSIEGWAEQNILVHLKPVEKCWQAQDFLPDPASEGFDEQVKEL 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVREL 111
                                                                                          oil-seeds with modified levels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tinctorius desaturase from clone pCGN2754
                                                                                                                                                                                                                                                     Thompson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       saturation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                               90US-0567373.
90US-0615784.
91WO-US01746.
95US-0471791.
                                                                                                                                                                                                                                                                                                                                                                                                                                          90US-0494106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0762762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             95US-0471791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= signal
34..396
/label= desatur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
represents a Carthamus tinctorius
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          safflower; delta-9 desaturase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    desaturase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B
                                                                                          of
                                                                                          fatty acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            oilseed;
desaturase
                                                                                          saturation
from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  176
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99999999888
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Best Local Sim
Matches 271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            clone pCGN2754. The present invention describes a recombinant DNA construct comprising a DNA sequence encoding a plant Delta-9 desaturase protein. The present invention also provides a method of modifying fatty acid composition in a host plant cell from a given fatty acid saturation to a different fatty acid saturation, comprising growing a host plant cell containing a recombinant DNA sequence which encodes a plant desaturate under the control of regulatory elements functional in the plant cell during lipid accumulation. Also, oilseeds having a modified level of fatty acid saturation and oils produced from such oilseeds.
                                                                                                                                                                             Glycine
                                                                                                                                                                                                       Stearoyl-ACP-desaturase; fatty acid; stearic acid;
11-DEC-1992;
                         25-MAY-1990;
                                                                                                                 Protein
                                                                                                                                                                                                                                           Stearoyl-ACP-desaturase precursor
                                                                                                                                                                                                                                                                      10-APR-1996
                                                                                                                                                                                                                                                                                                                         AAR82024 standard; Protein; 391 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                  22-AUG-1995
                                                                                                                                         Peptide
                                                                          JS5443974-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 MALKL---NFQCKKNHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QEYVCELGPKIRRVEEKVQGKEKKKKAEHP-VSFSWIFNRELKI 394
                                                                                                                                                                                                                                                                                                                                                                                                                                        ANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GNTARHAKDHGDVKLAQICGTIASDEKRHETAYTKIVEKLFEIDPDGTVLAFADMMRKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRHGDLLHTYLYLSGRVDMRQIQKTIQYLIGSGMDPRTENSPYLGFIYTSFQERATFVSH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VHVQVTHSMPPQKIEIFKSTEGWAEQNILVHLKPVEKCWQAQDFLPDPASEGFDEQVKEL
                                                                                                                                                                                                                                                                                                                                                                                         QDYVCGLPPRIRRLEERAQGRAK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFISH 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MALRITPVTLQSERYRSFSFPKK----ANLRSPKFAMASTLGSSTPKVDNAKKPFQPPRE
                                                                                                                                                                             max cv.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         396 AA;
                                                                                                                                                                                                       stearic acid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                      (first entry)
                         90US-0529049
                                                                                                                                                                               Wye.
                                                                                                               /label= Transit_peptide
                                                                                                                                                    Location/Qualifiers
                                                                                                    /label= Mat_protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.2%;
67.1%;
                                                                                                                                                                                                      soybean; seed oil; vegetable oil;
transgenic plant; crop improveme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 1406; DB 1
Pred. No. 2e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                         EGPVVPFSWIFDRQVKL 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61;
                                                                                                                                                                                                       improvement.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                          356
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92US-0995657

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RESULT 12
AAW14797
ID AAW14
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AC AAW14
XX
DT 03-JU
DT 03-JU
XX
DE Rapes
XX
KW Stear
KW antis
KW veget
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VS
SS Brass
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Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The stearoyl-ACP-desaturase precursor (AAR82024) is the product of a cDNA clone (AAR00395) derived from soybean developing leaves. It catalyses the conversion of stearoyl-ACP to oleoyl-ACP. Expression of the mature enzyme in transgenic plants such as soybean, rapeseed, sunflower, cocoa, peanut, sunflower and corn, allows the fatty acid composition, esp. the stearic acid content, of the seed oil fatty acid composition, esp. the stearic acid content, of the seed oil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-MAY-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      fatty
to be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated soybean stearoyl-ACP desaturase gene - use for the prodn. of seed oil contg. altered levels of satd. and unsatd. fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (DUPO)
                            Stearoyl-ACP desaturase; rapeseed; acyl-ACP thioesterase; antisense; triglyceride; stearic acid; transgenic plant; vegetable oil; mangosteen; Garcinia mangifera.
  Brassica
                                                                                                                 03-JUL-1997
                                                                                    Rapeseed
                                                                                                                                                                                                                                           347
                                                                                                                                                                                                                                                                      347
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                QVRELRERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRA 166
||:||||||| || ||||||||||||||:||| :||||| ::|||||
QVKELRERAKEITLXYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASLTSWAIWTRA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MALKLNFQCKKNHPAAFAKSPLPVTRVS-----SPRVFMASTVNSNSMVLDNLKSP-
                                                                                                                                                                                                                                                                                                  MRKKITMPAHLMYDGSDELLEKHETAVAQRVXVYSALDYCDILEELVDKWNVERLTGLSD 346
                                                                                                                                                                                                                                                                                                                                                     TFISHANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADM 286
                                                                                                                                                                                                                                                                                                                                                                                                             WTAEENRHGDLLNKYLYLSGRVDMKQIEKTIQYLIGSGMDPRTENSPYLGFIYTSFQERA
                                                                                                                                                                                                                                                                                                                                                                                                                           WTAEENRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERA 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TPPREVHVQVTHSMPPQKIEIFKSLEDWADQNILTHLKPVEKCWQPQDFLPNPSSDGFEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEE 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MALRLN------PIPTQTFSLPQMPSLRSPRFRMASTLRSGSKEVENIKKPF 46
                                                                                                                                                                                                                                           EGRKAQEYVCGLPPRIRRLEERAQARGKESST---LKFSWIHDREV
                                                                                                                                                                                                                                                          EGRKAQEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNREL 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      controlled.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DU PONT DE NEMOURS & CO
  napus cv.
                                                                                                                                                                      standard; Protein;
                                                                                     stearoyl-ACP desaturase BND11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perez-Grau
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Column 41-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    90US-0529049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68.1%;
                                                                                                                 entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        45;
                                                                                                                                                                         401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1404.5;
Pred. No. 2.76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ħ
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                                             transgenic plant; oilseed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .7e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        56;
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                                                                                                                                                                                                                                              389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    391;
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Db QУ

Qy

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Qy

Qγ

B

Qy Db γQ DЬ

B

RESULT 13
AAR14190
ID AAR14
XX
AC AAR14

AAR14190 standard;

Protein;

398

AA

AAR14190

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Query Match
Best Local S
Matches 265
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AAW14798) each catalyse the desaturation of stearcy1-ACP (C18:0) to oleoy1-ACP (C18:1). Their amino acid sequences were deduced from cDNA clones (AAT63437-38) isolated from a Brassica napus cv. 212/86 mid-mturation seed cDNA library. An antisense gene was constructed to generate antisense RNA homologous to both BND9 and BND11. In transgenic Brassica plants expressing the stearcy1-ACP desaturase antisense construct and mangosteen Class I acy1-ACP thioesterase GarmfatA1 (see also AAW14795), levels of C18:0 in the seed oil may exceed 50% of total fatty acids.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Increasing levels of using a DNA sequence substantial activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (CALJ ) CALGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            30-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-APR-1997.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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 360
                               350
                                                              300
                                                                                                                           240
                                                                                                                                                          230
                                                                                                                                                                                        180
                                                                                                                                                                                                                      170
                                                                                                                                                                                                                                                     120
                                                                                                                                                                                                                                                                                  110
                                                                                             290
                                                                                                                                                                                                                                                                                                              60
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                                                                                                                                                                                                                                                                                                                                                                           Н
                                                                                                                                                                                                                                                                                                                                                                                                       1 MALKLNFQCKKNHPAAFAKSPLPVTRVSSPR-VFMAST----VNSNSMVLDNLKSP----
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DB; AAT63437.
                                                           KAQEYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI 394
                                                                                                                                                                                   KEVHVQVLHSMPPQKIEIFKSMEDWAEHNLLPHLKDVEKSWQPQDFLPDPASDGFEDQVK 119
                                                                                                                                                                                                                                                                                                                             --PNLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVR 109
                                                                                                                                                                                                                                                                                                                                                                           MALKINPLASOPYKLPSSARP-PISTLRSPKFLCLASSSSPALSSSTKEVESLKKPFTPP
SHGNTARQAKEHGDLKLAQICGTIAADEKRHETAYTKIVEKLLEIDPDGTVVAFADMMRK
                                                                                                                                          SHANTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRK 289
                                                                                                                                                                                                       EENRHGDLLNKYLYLSGRVDMRKIEKTIQYLIGSGMDIKSENSPYLGFIYTSFQERATFI 229
                                                                                                                                                                                                                                                   ELRERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTA 169
                                                                                                                                                                                                                                                                                                                                                                                                                                          265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5; Fig6A-6C; 55pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     401
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                95US-0537083
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       f stearate
encoding
on Cl8:0
                                                                                                                                                                                                                                                                                                                                                                                                                                                       67.98;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1400.5;
Pred. No. 6.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        e in plant
g acyl-ACP
d acyl-ACP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MW
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seed triglyceride(s)
thioesterase protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            substrates
                                                                                                                                                                                                                                                                                                                                                                                                                                                       .5; DB 18;
5.9e-126;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
      401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 401;
                                                                                                                                                                                                                                                                                                                                                                                                                                ± 15;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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11-DEC-1991

(first entry)

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                                                                                                                                                                                                                                                     Query Match
Best Local :
                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                        increased percentage of unsatd. fatty acids may be provided, using anti-sense technology, the amt. of desaturase can be decreased, resulting in a higher percentage of fatty acids.
Using the desaturase gene and derivs. in cells and plants, desirable traits such as chill tolerance may be introduced and environmentally safe herbicide prods. may be provided.
                                                                                                                                                                                                                                                                                                                                                                                               Modification of fatty acid in a plant host cell to a different percentage of fatty acid sath. is possible by growing a host plant cell having integrated into its genome a recombinant DNA sequence encoding this protein, under the control of regulatory elements functional in the plant cell during lipid accumulation, under conditions which will promote the activity of the regulatory elements. By increasing the amt. of desaturase available in plant cells, an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1991-295627/40.
N-PSDB; AAQ13965.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-NOV-1990;
16-MAR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica campestris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Desaturase;
herbicide.
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fatty acid compsn. of plant cells and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DNA encoding a plant desaturase - used for modifying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CALG-) CALGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13-AUG-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14-MAR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-SEP-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9113972-A.
 240
                        233
                                                                      173
                                                                                              120
                                                                                                                     113
                                                180
                                                                                                                                             60
                                                                                                                                                                    53
                                                                                                                                                                                        campestris delta9 desaturase from pCGN3235
                                                                                                                                                                                                                                                                                                                  also AAQ13963-69.
                                            NTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKIT
                                                                                                       ERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEEN 172
                                                                                                                                           ERARELPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAEEN
                                                                                                                                                                 NLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELR 112
NTARQAKEHGDLKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVMAFADMMRKKIS
                                                                                                                                                                                                                                            269;
                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   رە
                                                                                                                                                                                                                                                                                          398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fig 4C;
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fatty
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Knauf V;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90US-0615784.
90US-0494106.
90US-0567373.
                                                                                                                                                                                                                                                                                          AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91WO-UO01746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid; saturation; chill tolerance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 128pp;
                                                                                                                                                                                                                                                     67.7%;
                                                                                                                                                                                                                                         55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English
                                                                                                                                                                                                                                                     Score 1396; DB 12;
Pred. No. 1.8e-125;
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plant seeds
                                                                                                                                                                                                                                         66;
                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                         Indels
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                                                                                                                                                                                                                                                                  398;
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299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
                                                                                                                                                                      Query Match
Best Local :
                                                                                                                                                       Matches
                                                                                                                                                                                                                                                    mid-mturation seed cDNA library. An antisense gene was constructed to generate antisense RNA homologous to both BND9 and BND11. In transgenic Brassica plants expressing the stearoyl-ACP desaturase antisense construct and mangosteen Class I acyl-ACP thioesterase GarmFatAl (see also AAM14795), levels of C18:0 in the seed oil may
                                                                                                                                                                                                                                                                                                           (AAW41798) each catalyse the desaturation of stearoy1-ACP (C18:0) to oleoy1-ACP (C18:1). Their amino acid sequences were deduced from cDNA clones (AAT63437-38) isolated from a Brassica napus cv. 212/86 mid-mturation seed cDNA library. An antisense gene was constructed
                                                                                                                                                                                                                                                                                                                                                                                                                             using a DNA sequence substantial activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stearoyl-ACP desaturase; rapeseed; acyl-ACP thioesterase; antisense; triglyceride; stearic acid; transgenic plant;
                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                        Oilseed
                                                                                                                                                                                                                                                                                                                                                                                                                                         Increasing levels of using a DNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Knauf VC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAW14798;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW14798 standard;
                                                                                                                                                                                                                                           exceed
                                                                                                                                                                                                                                                                                                                                                                                                 Example 5; Fig7A-7C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-SEP-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-APR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO9712047-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 vegetable oil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rapeseed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CALJ ) CALGENE INC
              113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               353
                                          60
                                                                    53
                                                                                                                           1 MALKLNFQCKKNHPAAFAKSPLPVTRVSSPR--VFMASTVNSNSMVLDNLKSP-----P 52
              ERAKEIPDDYFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEEN
                                                                  NLQVTHSMPPQKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1997-212906/19.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPAHLMYDGSDELLFKHFTAVAQRVXVYSALDYCDILEFLVDKWNVERLTGLSDEGRKAQ
                                         HVQVLHSMPPQKIEIFKSMEDWAEQNLLTQLKDVEKSWQPQDFLPDPASDGFEDQVRELR 119
                                                                                                MALKLNPLASQPYNFPSSARP-PVSTFRSPKFLCLASSSPALSSKEVESLKKPFTPPKEV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EYLCGLTPRIRRLDERAQARAKKGP---KVPFSWIHDREVQL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPAHLMYDGRDESLEDNESSVAQRLGVYTAKDYADILEELVGRWKIESLTGLSGEGNKAQ
269;
                                                                                                                                                                                                                                          50%
                                                                                                                                                                                                                                                                                                                                                                      rape stearoyl-ACP desaturases BND11 (AAW14797) and BND9
                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAT63438.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          stearoyl-ACP desaturase BND9
                                                                                                                                                                                                                                          of total
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kridl J,
                                                                                                                                                                                                               398
                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                               ĀĀ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mangosteen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95US-0537083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96WO-US16078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212/86.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                                                                   67.7%;
                                                                                                                                                                                                                                          fatty acids.
                                                                                                                                                                                                                                                                                                                                                                                                                          stearate in plant seed triglyceride(s) encoding acyl-ACP thioesterase protein on C18:0 acyl-ACP substrates
                                                                                                                                                                                                                                                                                                                                                                                                55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Lassner
                                                                                                                                                       55;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Garcinia mangifera
                                                                                                                                                     Score 1396; DB 18;
Pred. No. 1.8e-125;
5; Mismatches 66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              398
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394
                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oilseed;
                                                                                                                                                       12;
                                                                                                                                                                                                                                                                                                                                                                                                                                           having
                                                                                                                                                     Gaps
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RESULT 15
AAW444351
ID AAW444351
AC AAW44
XX AAW44
XX AAW44
XX AAW44
XX AW44
XX Brass
XX D6-J
PD 03-M
PD 06-J
XX Brass
XX D6-J
PR 14-M
PR 16-M
PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1991;
16-MAR-1990;
13-AUG-1990;
14-NOV-1990;
14-MAR-1991;
06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW44351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAW44351 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     03-MAR-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5723595-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brassica campestris; confatty acid saturation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Brassica campestris desaturase from clone pCGN3235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-MAY-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240
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                                        construct comprising a DNA sequence encoding a plant Delta-9 desaturase protein. The present invention also provides a method of modifying fatty acid composition in a host plant cell from a given fatty acid saturation to a different fatty acid saturation, comprising growing a host plant cell containing a recombinant DNA sequence which encodes a plant desaturase under the control of regulatory elements functional in the plant cell during lipid accumulation. Also, oilseeds having a modified level of fatty acid saturation and oils produced from such oilseeds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        293
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                                                                                                                                                                                                                                                                                                                                                                                      DNA encoding plant delta-9 desaturase protein - having amino acid sequence of Carthamus tinctorius desaturase, useful for, e.g. producing oil-seeds with modified levels of fatty acid saturation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Knauf VC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    360
                                                                                                                                                                                                                                                          The present sequence represents a Brassica campestris desaturase from clone pCGN3235. The present invention describes a recombinant DNA
                                                                                                                                                                                                                                                                                                                                        Claim 9; Column 63-66; 87pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (CALJ ) CALGENE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKIT
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EYLCGLTPRIRRLDERAQARAKKGP---KVPFSWIHDREVQL 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1998-178544/16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAV15253.
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          398
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90US-0567373.
90US-0615784.
91WO-US01746.
95US-0471791.
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          AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oilseed;
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Sequence

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                                                                                                                                                                                                                                                                        Local
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                   353
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360
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                                                                                                                                                                                                                                             MALKLNFQCKK--NHPAAFAKSPLPVTRVSSPRVFMASTVNSNSMVLDNLKSP-----P
                                                                                                                                                                                                                            NTARQAKEHGDLKLAQICGTIAADEKRHETAYTKIVEKLFEIDPDGTVMAFADMMRKKIS
                                                                                   NTAKLAQHYGDKNLAHICGSIASDEKRHATAYTKIVEKLAEIDPDTTVIAFADMMRKKIT
                                                                                                            ERARELPDDYFVVLVGDMITEEALPTYQTMLNTLDGVRDETGASPTSWAIWTRAWTAEEN
                                                                                                                                                            ERAKBIPDDXFVVLVGDMITEEALPTYMSMLNRCDGIKDETGAEPSAWAMWTRAWTAEEN 172
                                                                                                                                                                                      HYQYLHSMPPQKIEIFKSMEDWAEQNLLTQLKDVEKSWQPQDFLPDPASDGFEDQVRELR
                                                                                                                                                                                                NLQVTHSMPPOKLEIFKSLDDWARNNVLIHLKSVEKSWQPQDYLPDPVSDGFEEQVRELR 112
                 EYVCELGPKIRRVEEKVQGKEKKKKAEHPVSFSWIFNRELKI 394
EYLCGLTPRIRRLDERAQARAKKGP---KVPFSWIHDREVQL
                                                                                                                                                                                                                                                                al Similarity
269; Conserv
                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                           Score 1396;
Pred. No. 1
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                                                                                                                                                                                                                                                                                      DB 19;
                                                                                                                                                                                                                                                                                       Length
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Search completed: December Job time : 41 secs 2002, 21:20:14

4	4	4	4	41	4	ω	ω	ω	u	ω	ų	ω	3	ω	w
5 99		3 99.5								5 104.5					
. 4.8	4.8	4.8	4.8	4.9	4.9	4.9	5.0	5.0	5.0	5.1	5.1	5.1	5.1	5.1	5.1
782	1120	517	604	3643	1027	846	520	393	244	570	524	684	520	520	393
2	N	N	N	N	N	N	N	Ν	N	Ν	N	N	N	N	N
A82940	JC7765	T48283	T19682	T36410	T46296	JC7720	S49395	F64679	C89811	T30156	T43050	AE2004	A99566	F90596	C71836
lkų	mit	an)	lyh	pro	hyı	ace	HSO	try	hyp	hyp	сус	hyp	res	res	try
hypothetical prote	itotic spindle as	nkyrin-like prote	ypothetical prote	robable polyketid	ypothetical prote	acetyltransferase	1sdM1 protein - My	yptophan synthas	/pothetical prote	ypothetical prote	yclin E - Caenorh	/pothetical prote	estriction modifi	estriction-modifi	ryptophan synthas

ALIGNMENTS

RESULT A47245

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